Document made available under the Patent Cooperation Treaty (PCT)

International application number: PCT/US2004/026361

International filing date: 13 August 2004 (13.08.2004)

Document type: Certified copy of priority document

Document details: Country/Office: US
Number: 60/495,172
Filing date: 14 August 2003 (14.08.2003)

Date of receipt at the International Bureau: 19 February 2007 (19.02.2007)

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b)

World Intellectual Property Organization (WIPO) - Geneva, Switzerland
Organisation Mondiale de la Propriété Intellectuelle (OMPI) - Genève, Suisse

1576686

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE

United States Patent and Trademark Office

February 12, 2007

THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE.

APPLICATION NUMBER: ***60/495,172***
FILING DATE: ***August 14, 2003***
RELATED PCT APPLICATION NUMBER: ***PCT/US04/26361***

THE COUNTRY CODE AND NUMBER OF YOUR PRIORITY APPLICATION, TO BE USED FOR FILING ABROAD UNDER THE PARIS CONVENTION, IS ***US60/495,172***

UNITED STATES PATENT AND TRADEMARK OFFICE
DEPARTMENT OF COMMERCE

Certified by

Jon W. Dudas

Under Secretary of Commerce
for Intellectual Property
and Director of the United States
Patent and Trademark Office

16623 U.S. PTO 08/14/03

19704 U.S. PTO 60/495172 08/14/03

PTO/SB/16 (05-03)
Approved for use through 4/30/2003. OMB 0651-0032
U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request f r filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53 (c).

Express Mail Label N . EV342494129US

INVENTOR(S)		
Given Name (first and middle [if any])	Family Name or Surname	Residence (City and either State or Foreign Country)
Helen	Francis -Lang	San Francisco, California
Christopher G.	Winter	Palo Alto, California

☒ *Additional inventors are being named on the* 1 *separately numbered sheets attached hereto*

TITLE OF THE INVENTION (500 characters max)

MBCATs as Modifiers of the Beta-Catenin Pathway and Methods of Use

CORRESPONDENCE ADDRESS

Direct all correspondence to:

☒ Customer Number: 23500 (*Type Customer Number here*) → *Place Customer Number Bar Code Label here*

OR

☐ Firm or Individual Name					
Address					
Address					
City		State		ZIP	
Country		Telephone		Fax	

ENCLOSED APPLICATION PARTS *(check all that apply)*

☒ Specification *Number of Pages* 104

☐ CD(s), Number

☐ Drawing(s) *Number of Sheets*

☒ Other (specify) return receipt postcard

☐ Application Data Sheet. See 37 CFR 1.76

METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT

☐ Applicant claims small entity status. See 37 CFR 1.27.

☐ A check or money order is enclosed to cover the filing fees

☒ The Director is hereby authorized to charge filing fees or credit any overpayment to Deposit Account Number: 50-1108

FILING FEE AMOUNT ($): 160

☐ Payment by credit card. Form PTO-2038 is attached.

The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.

☒ No.

☐ Yes, the name of the U.S. Government agency and the Government contract number are: _____.

Respectfully submitted,

SIGNATURE [signature]

Date 8/14/2003

TYPED or PRINTED NAME Laleh Shayesteh

REGISTRATION NO. *(if appropriate)* 47,937

Docket Number: EX03-053P

TELEPHONE 650.837.8223

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

PROVISIONAL APPLICATION COVER SHEET
Additional Page

PTO/SB/16 (05-03)
Approved for use through 4/30/2003. OMB 0651-0032
Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE
Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

Docket Number	EX03-053P

INVENTOR(S)/APPLICANT(S)		
Given Name (first and middle [if any])	Family or Surname	Residence (City and either State or Foreign Country)
Richard Benn Abegania	Ventura	Daly City, California
Lynn Margaret	Bjerke	San Francisco, California
Kim	Lickteig	San Francisco, California
Joanne I.	Adamkewicz	San Francisco, California
HaiGuang	Zhang	El Sobrante, California
Bing	Hai	Redwood City, California

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

MBCATs AS MODIFIERS OF THE BETA-CATENIN PATHWAY AND METHODS OF USE

BACKGROUND OF THE INVENTION

The *Drosophila Melanogaster* Armadillo/beta-catenin protein is implicated in multiple cellular functions. The protein functions in cell signaling via the Wingless (Wg)/Wnt signaling pathway. It also functions as a cell adhesion protein at the cell membrane in a complex with E-cadherin and alpha-catenin (Cox et al. (1996) J. Cell Biol. 134: 133-148; Godt and Tepass (1998) Nature 395: 387-391; White et al. (1998) J Cell biol. 140:183-195). These two roles of beta -catenin can be separated from each other (Orsulic and Peifer (1996) J. Cell Biol. 134: 1283-1300; Sanson et al. (1996) Nature 383: 627-630).

In Wingless cell signaling, beta -catenin levels are tightly regulated by a complex containing APC, Axin, and GSK3 beta /SGG/ZW3 (Peifer et al. (1994) Development 120: 369-380).

The Wingless/ beta -catenin signaling pathway is frequently mutated in human cancers, particularly those of the colon. Mutations in the tumor suppressor gene APC, as well as point mutations in beta -catenin itself lead to the stabilization of the beta -catenin protein and inappropriate activation of this pathway.

The ability to manipulate the genomes of model organisms such as *Drosophila* provides a powerful means to analyze biochemical processes that, due to significant evolutionary conservation, have direct relevance to more complex vertebrate organisms. Due to a high level of gene and pathway conservation, the strong similarity of cellular processes, and the functional conservation of genes between these model organisms and mammals, identification of the involvement of novel genes in particular pathways and their functions in such model organisms can directly contribute to the understanding of the correlative pathways and methods of modulating them in mammals (see, for example, Mechler BM et al., 1985 EMBO J 4:1551-1557; Gateff E. 1982 Adv. Cancer Res. 37: 33-74; Watson KL., et al., 1994 J Cell Sci. 18: 19-33; Miklos GL, and Rubin GM. 1996 Cell 86:521-529; Wassarman DA, et al., 1995 Curr Opin Gen Dev 5: 44-50; and Booth DR. 1999 Cancer

Metastasis Rev. 18: 261-284). For example, a genetic screen can be carried out in an invertebrate model organism having underexpression (e.g. knockout) or overexpression of a gene (referred to as a "genetic entry point") that yields a visible phenotype. Additional genes are mutated in a random or targeted manner. When a gene mutation changes the original phenotype caused by the mutation in the genetic entry point, the gene is identified as a "modifier" involved in the same or overlapping pathway as the genetic entry point. When the genetic entry point is an ortholog of a human gene implicated in a disease pathway, such as beta-catenin, modifier genes can be identified that may be attractive candidate targets for novel therapeutics.

All references cited herein, including patents, patent applications, publications, and sequence information in referenced Genbank identifier numbers, are incorporated herein in their entireties.

SUMMARY OF THE INVENTION

We have discovered genes that modify the beta-catenin pathway in *Drosophila*, and identified their human orthologs, hereinafter referred to as modifier of beta catenin (MBCAT). The invention provides methods for utilizing these beta-catenin modifier genes and polypeptides to identify MBCAT-modulating agents that are candidate therapeutic agents that can be used in the treatment of disorders associated with defective or impaired beta-catenin function and/or MBCAT function. Preferred MBCAT-modulating agents specifically bind to MBCAT polypeptides and restore beta-catenin function. Other preferred MBCAT-modulating agents are nucleic acid modulators such as antisense oligomers and RNAi that repress MBCAT gene expression or product activity by, for example, binding to and inhibiting the respective nucleic acid (i.e. DNA or mRNA).

MBCAT modulating agents may be evaluated by any convenient *in vitro* or *in vivo* assay for molecular interaction with an MBCAT polypeptide or nucleic acid. In one embodiment, candidate MBCAT modulating agents are tested with an assay system comprising a MBCAT polypeptide or nucleic acid. Agents that produce a change in the activity of the assay system relative to controls are identified as candidate beta-catenin modulating agents. The assay system may be cell-based or

cell-free. MBCAT-modulating agents include MBCAT related proteins (e.g. dominant negative mutants, and biotherapeutics); MBCAT -specific antibodies; MBCAT -specific antisense oligomers and other nucleic acid modulators; and chemical agents that specifically bind to or interact with MBCAT or compete with MBCAT binding partner (e.g. by binding to an MBCAT binding partner). In one specific embodiment, a small molecule modulator is identified using a binding assay. In specific embodiments, the screening assay system is selected from an apoptosis assay, a cell proliferation assay, an angiogenesis assay, and a hypoxic induction assay.

In another embodiment, candidate beta-catenin pathway modulating agents are further tested using a second assay system that detects changes in the beta-catenin pathway, such as angiogenic, apoptotic, or cell proliferation changes produced by the originally identified candidate agent or an agent derived from the original agent. The second assay system may use cultured cells or non-human animals. In specific embodiments, the secondary assay system uses non-human animals, including animals predetermined to have a disease or disorder implicating the beta-catenin pathway, such as an angiogenic, apoptotic, or cell proliferation disorder (e.g. cancer).

The invention further provides methods for modulating the MBCAT function and/or the beta-catenin pathway in a mammalian cell by contacting the mammalian cell with an agent that specifically binds a MBCAT polypeptide or nucleic acid. The agent may be a small molecule modulator, a nucleic acid modulator, or an antibody and may be administered to a mammalian animal predetermined to have a pathology associated the beta-catenin pathway.

DETAILED DESCRIPTION OF THE INVENTION

In a screen to identify enhancers and suppressors of the Wg signaling pathway, we generated activated beta -catenin models in *Drosophila* based on human tumor data (Polakis (2000) Genes and Development 14: 1837-1851). We identified modifiers of the Wg pathway and identified their orthologs. Accordingly, vertebrate orthologs of these modifiers, and preferably the human orthologs, MBCAT genes (i.e., nucleic acids and polypeptides) are attractive drug targets for the treatment of pathologies associated with a

defective beta-catenin signaling pathway, such as cancer. Table 1 (Example II) lists the modifiers and their orthologs.

In vitro and in vivo methods of assessing MBCAT function are provided herein. Modulation of the MBCAT or their respective binding partners is useful for understanding the association of the beta-catenin pathway and its members in normal and disease conditions and for developing diagnostics and therapeutic modalities for beta-catenin related pathologies. MBCAT-modulating agents that act by inhibiting or enhancing MBCAT expression, directly or indirectly, for example, by affecting an MBCAT function such as enzymatic (e.g., catalytic) or binding activity, can be identified using methods provided herein. MBCAT modulating agents are useful in diagnosis, therapy and pharmaceutical development.

Nucleic acids and polypeptides of the invention

Sequences related to MBCAT nucleic acids and polypeptides that can be used in the invention are disclosed in Genbank (referenced by Genbank identifier (GI) or RefSeq number), shown in Table 1 and in the appended sequence listing.

The term "MBCAT polypeptide" refers to a full-length MBCAT protein or a functionally active fragment or derivative thereof. A "functionally active" MBCAT fragment or derivative exhibits one or more functional activities associated with a full-length, wild-type MBCAT protein, such as antigenic or immunogenic activity, enzymatic activity, ability to bind natural cellular substrates, etc. The functional activity of MBCAT proteins, derivatives and fragments can be assayed by various methods known to one skilled in the art (Current Protocols in Protein Science (1998) Coligan *et al.*, eds., John Wiley & Sons, Inc., Somerset, New Jersey) and as further discussed below. In one embodiment, a functionally active MBCAT polypeptide is a MBCAT derivative capable of rescuing defective endogenous MBCAT activity, such as in cell based or animal assays; the rescuing derivative may be from the same or a different species. For purposes herein, functionally active fragments also include those fragments that comprise one or more structural domains of an MBCAT, such as a kinase domain or a binding domain. Protein domains can be identified using the PFAM program (Bateman A., et al., Nucleic Acids Res, 1999, 27:260-2). Methods

for obtaining MBCAT polypeptides are also further described below. In some embodiments, preferred fragments are functionally active, domain-containing fragments comprising at least 25 contiguous amino acids, preferably at least 50, more preferably 75, and most preferably at least 100 contiguous amino acids of an MBCAT. In further preferred embodiments, the fragment comprises the entire functionally active domain.

The term "MBCAT nucleic acid" refers to a DNA or RNA molecule that encodes a MBCAT polypeptide. Preferably, the MBCAT polypeptide or nucleic acid or fragment thereof is from a human, but can also be an ortholog, or derivative thereof with at least 70% sequence identity, preferably at least 80%, more preferably 85%, still more preferably 90%, and most preferably at least 95% sequence identity with human MBCAT. Methods of identifying orthlogs are known in the art. Normally, orthologs in different species retain the same function, due to presence of one or more protein motifs and/or 3-dimensional structures. Orthologs are generally identified by sequence homology analysis, such as BLAST analysis, usually using protein bait sequences. Sequences are assigned as a potential ortholog if the best hit sequence from the forward BLAST result retrieves the original query sequence in the reverse BLAST (Huynen MA and Bork P, Proc Natl Acad Sci (1998) 95:5849-5856; Huynen MA *et al.*, Genome Research (2000) 10:1204-1210). Programs for multiple sequence alignment, such as CLUSTAL (Thompson JD et al, 1994, Nucleic Acids Res 22:4673-4680) may be used to highlight conserved regions and/or residues of orthologous proteins and to generate phylogenetic trees. In a phylogenetic tree representing multiple homologous sequences from diverse species (e.g., retrieved through BLAST analysis), orthologous sequences from two species generally appear closest on the tree with respect to all other sequences from these two species. Structural threading or other analysis of protein folding (e.g., using software by ProCeryon, Biosciences, Salzburg, Austria) may also identify potential orthologs. In evolution, when a gene duplication event follows speciation, a single gene in one species, such as *Drosophila*, may correspond to multiple genes (paralogs) in another, such as human. As used herein, the term "orthologs" encompasses paralogs. As used herein, "percent (%) sequence identity" with respect to a subject sequence, or a

specified portion of a subject sequence, is defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1997) 215:403-410) with all the search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A % identity value is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported. "Percent (%) amino acid sequence similarity" is determined by doing the same calculation as for determining % amino acid sequence identity, but including conservative amino acid substitutions in addition to identical amino acids in the computation.

A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid having similar properties such that the folding or activity of the protein is not significantly affected. Aromatic amino acids that can be substituted for each other are phenylalanine, tryptophan, and tyrosine; interchangeable hydrophobic amino acids are leucine, isoleucine, methionine, and valine; interchangeable polar amino acids are glutamine and asparagine; interchangeable basic amino acids are arginine, lysine and histidine; interchangeable acidic amino acids are aspartic acid and glutamic acid; and interchangeable small amino acids are alanine, serine, threonine, cysteine and glycine.

Alternatively, an alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman (Smith and Waterman, 1981, Advances in Applied Mathematics 2:482-489; database: European Bioinformatics Institute; Smith and Waterman, 1981, J. of Molec.Biol., 147:195-197; Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.psc.edu) and references cited therein.; W.R. Pearson, 1991, Genomics 11:635-650). This algorithm can be applied to amino acid sequences by using the scoring

matrix developed by Dayhoff (Dayhoff: Atlas of Protein Sequences and Structure, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA), and normalized by Gribskov (Gribskov 1986 Nucl. Acids Res. 14(6):6745-6763). The Smith-Waterman algorithm may be employed where default parameters are used for scoring (for example, gap open penalty of 12, gap extension penalty of two). From the data generated, the "Match" value reflects "sequence identity."

Derivative nucleic acid molecules of the subject nucleic acid molecules include sequences that hybridize to the nucleic acid sequence of an MBCAT. The stringency of hybridization can be controlled by temperature, ionic strength, pH, and the presence of denaturing agents such as formamide during hybridization and washing. Conditions routinely used are set out in readily available procedure texts (*e.g.*, Current Protocol in Molecular Biology, Vol. 1, Chap. 2.10, John Wiley & Sons, Publishers (1994); Sambrook *et al.*, Molecular Cloning, Cold Spring Harbor (1989)). In some embodiments, a nucleic acid molecule of the invention is capable of hybridizing to a nucleic acid molecule containing the nucleotide sequence of an MBCAT under high stringency hybridization conditions that are: prehybridization of filters containing nucleic acid for 8 hours to overnight at 65° C in a solution comprising 6X single strength citrate (SSC) (1X SSC is 0.15 M NaCl, 0.015 M Na citrate; pH 7.0), 5X Denhardt's solution, 0.05% sodium pyrophosphate and 100 μg/ml herring sperm DNA; hybridization for 18-20 hours at 65° C in a solution containing 6X SSC, 1X Denhardt's solution, 100 μg/ml yeast tRNA and 0.05% sodium pyrophosphate; and washing of filters at 65° C for 1h in a solution containing 0.1X SSC and 0.1% SDS (sodium dodecyl sulfate).

In other embodiments, moderately stringent hybridization conditions are used that are: pretreatment of filters containing nucleic acid for 6 h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 μg/ml denatured salmon sperm DNA; hybridization for 18-20h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100

μg/ml salmon sperm DNA, and 10% (wt/vol) dextran sulfate; followed by washing twice for 1 hour at 55° C in a solution containing 2X SSC and 0.1% SDS.

Alternatively, low stringency conditions can be used that are: incubation for 8 hours to overnight at 37° C in a solution comprising 20% formamide, 5 x SSC, 50 mM sodium phosphate (pH 7.6), 5X Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured sheared salmon sperm DNA; hybridization in the same buffer for 18 to 20 hours; and washing of filters in 1 x SSC at about 37° C for 1 hour.

Isolation, Production, Expression, and Mis-expression of MBCAT Nucleic Acids and Polypeptides

MBCAT nucleic acids and polypeptides, are useful for identifying and testing agents that modulate MBCAT function and for other applications related to the involvement of MBCAT in the beta-catenin pathway. MBCAT nucleic acids and derivatives and orthologs thereof may be obtained using any available method. For instance, techniques for isolating cDNA or genomic DNA sequences of interest by screening DNA libraries or by using polymerase chain reaction (PCR) are well known in the art. In general, the particular use for the protein will dictate the particulars of expression, production, and purification methods. For instance, production of proteins for use in screening for modulating agents may require methods that preserve specific biological activities of these proteins, whereas production of proteins for antibody generation may require structural integrity of particular epitopes. Expression of proteins to be purified for screening or antibody production may require the addition of specific tags (*e.g.*, generation of fusion proteins). Overexpression of an MBCAT protein for assays used to assess MBCAT function, such as involvement in cell cycle regulation or hypoxic response, may require expression in eukaryotic cell lines capable of these cellular activities. Techniques for the expression, production, and purification of proteins are well known in the art; any suitable means therefore may be used (e.g., Higgins SJ and Hames BD (eds.) Protein Expression: A Practical Approach, Oxford University Press Inc., New York 1999; Stanbury PF et al., Principles of Fermentation Technology, 2nd edition, Elsevier Science, New York, 1995; Doonan S (ed.) Protein Purification Protocols, Humana

Press, New Jersey, 1996; Coligan JE et al, Current Protocols in Protein Science (eds.), 1999, John Wiley & Sons, New York). In particular embodiments, recombinant MBCAT is expressed in a cell line known to have defective beta-catenin function. The recombinant cells are used in cell-based screening assay systems of the invention, as described further below.

The nucleotide sequence encoding an MBCAT polypeptide can be inserted into any appropriate expression vector. The necessary transcriptional and translational signals, including promoter/enhancer element, can derive from the native MBCAT gene and/or its flanking regions or can be heterologous. A variety of host-vector expression systems may be utilized, such as mammalian cell systems infected with virus (*e.g.* vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.* baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, plasmid, or cosmid DNA. An isolated host cell strain that modulates the expression of, modifies, and/or specifically processes the gene product may be used.

To detect expression of the MBCAT gene product, the expression vector can comprise a promoter operably linked to an MBCAT gene nucleic acid, one or more origins of replication, and, one or more selectable markers (*e.g.* thymidine kinase activity, resistance to antibiotics, *etc.*). Alternatively, recombinant expression vectors can be identified by assaying for the expression of the MBCAT gene product based on the physical or functional properties of the MBCAT protein in *in vitro* assay systems (*e.g.* immunoassays).

The MBCAT protein, fragment, or derivative may be optionally expressed as a fusion, or chimeric protein product (i.e. it is joined via a peptide bond to a heterologous protein sequence of a different protein), for example to facilitate purification or detection. A chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other using standard methods and expressing the chimeric product. A chimeric product may also be made by protein synthetic techniques, *e.g.* by use of a peptide synthesizer (Hunkapiller *et al.*, Nature (1984) 310:105-111).

Once a recombinant cell that expresses the MBCAT gene sequence is identified, the gene product can be isolated and purified using standard methods (*e.g.* ion exchange, affinity, and gel exclusion chromatography; centrifugation; differential solubility; electrophoresis). Alternatively, native MBCAT proteins can be purified from natural sources, by standard methods (*e.g.* immunoaffinity purification). Once a protein is obtained, it may be quantified and its activity measured by appropriate methods, such as immunoassay, bioassay, or other measurements of physical properties, such as crystallography.

The methods of this invention may also use cells that have been engineered for altered expression (mis-expression) of MBCAT or other genes associated with the beta-catenin pathway. As used herein, mis-expression encompasses ectopic expression, over-expression, under-expression, and non-expression (*e.g.* by gene knock-out or blocking expression that would otherwise normally occur).

Genetically modified animals

Animal models that have been genetically modified to alter MBCAT expression may be used in *in vivo* assays to test for activity of a candidate beta-catenin modulating agent, or to further assess the role of MBCAT in a beta-catenin pathway process such as apoptosis or cell proliferation. Preferably, the altered MBCAT expression results in a detectable phenotype, such as decreased or increased levels of cell proliferation, angiogenesis, or apoptosis compared to control animals having normal MBCAT expression. The genetically modified animal may additionally have altered beta-catenin expression (e.g. beta-catenin knockout). Preferred genetically modified animals are mammals such as primates, rodents (preferably mice or rats), among others. Preferred non-mammalian species include zebrafish, *C. elegans*, and *Drosophila*. Preferred genetically modified animals are transgenic animals having a heterologous nucleic acid sequence present as an extrachromosomal element in a portion of its cells, i.e. mosaic animals (see, for example, techniques described by Jakobovits, 1994, Curr. Biol. 4:761-763.) or stably integrated into its germ line DNA (i.e., in the genomic sequence of most or all of its cells). Heterologous nucleic acid is

introduced into the germ line of such transgenic animals by genetic manipulation of, for example, embryos or embryonic stem cells of the host animal.

Methods of making transgenic animals are well-known in the art (for transgenic mice see Brinster et al., Proc. Nat. Acad. Sci. USA 82: 4438-4442 (1985), U.S. Pat. Nos. 4,736,866 and 4,870,009, both by Leder et al., U.S. Pat. No. 4,873,191 by Wagner et al., and Hogan, B., Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); for particle bombardment see U.S. Pat. No., 4,945,050, by Sandford *et al.*; for transgenic *Drosophila* see Rubin and Spradling, Science (1982) 218:348-53 and U.S. Pat. No. 4,670,388; for transgenic insects see Berghammer A.J. *et al.*, A Universal Marker for Transgenic Insects (1999) Nature 402:370-371; for transgenic Zebrafish see Lin S., Transgenic Zebrafish, Methods Mol Biol. (2000);136:375-3830); for microinjection procedures for fish, amphibian eggs and birds see Houdebine and Chourrout, Experientia (1991) 47:897-905; for transgenic rats see Hammer *et al.*, Cell (1990) 63:1099-1112; and for culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection see, e.g., Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E. J. Robertson, ed., IRL Press (1987)). Clones of the nonhuman transgenic animals can be produced according to available methods (see Wilmut, I. *et al.* (1997) Nature 385:810-813; and PCT International Publication Nos. WO 97/07668 and WO 97/07669).

In one embodiment, the transgenic animal is a "knock-out" animal having a heterozygous or homozygous alteration in the sequence of an endogenous MBCAT gene that results in a decrease of MBCAT function, preferably such that MBCAT expression is undetectable or insignificant. Knock-out animals are typically generated by homologous recombination with a vector comprising a transgene having at least a portion of the gene to be knocked out. Typically a deletion, addition or substitution has been introduced into the transgene to functionally disrupt it. The transgene can be a human gene (e.g., from a human genomic clone) but more preferably is an ortholog of the human gene derived from the transgenic host species. For example, a mouse MBCAT gene is used to construct a homologous

recombination vector suitable for altering an endogenous MBCAT gene in the mouse genome. Detailed methodologies for homologous recombination in mice are available (see Capecchi, Science (1989) 244:1288-1292; Joyner *et al.*, Nature (1989) 338:153-156). Procedures for the production of non-rodent transgenic mammals and other animals are also available (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science (1989) 244:1281-1288; Simms *et al.*, Bio/Technology (1988) 6:179-183). In a preferred embodiment, knock-out animals, such as mice harboring a knockout of a specific gene, may be used to produce antibodies against the human counterpart of the gene that has been knocked out (Claesson MH et al., (1994) Scan J Immunol 40:257-264; Declerck PJ et al., (1995) J Biol Chem. 270:8397-400).

In another embodiment, the transgenic animal is a “knock-in” animal having an alteration in its genome that results in altered expression (e.g., increased (including ectopic) or decreased expression) of the MBCAT gene, e.g., by introduction of additional copies of MBCAT, or by operatively inserting a regulatory sequence that provides for altered expression of an endogenous copy of the MBCAT gene. Such regulatory sequences include inducible, tissue-specific, and constitutive promoters and enhancer elements. The knock-in can be homozygous or heterozygous.

Transgenic nonhuman animals can also be produced that contain selected systems allowing for regulated expression of the transgene. One example of such a system that may be produced is the cre/loxP recombinase system of bacteriophage P1 (Lakso *et al.*, PNAS (1992) 89:6232-6236; U.S. Pat. No. 4,959,317). If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase. Another example of a recombinase system is the FLP recombinase system of Saccharomyces cerevisiae (O'Gorman et al. (1991) Science 251:1351-1355; U.S. Pat. No. 5,654,182). In a preferred embodiment, both Cre-LoxP and Flp-Frt are used in the same system to regulate expression of the transgene, and for sequential deletion of vector sequences in the same cell (Sun X et al (2000) Nat Genet 25:83-6).

The genetically modified animals can be used in genetic studies to further elucidate the beta-catenin pathway, as animal models of disease and disorders implicating defective beta-catenin function, and for *in vivo* testing of candidate therapeutic agents, such as those identified in screens described below. The candidate therapeutic agents are administered to a genetically modified animal having altered MBCAT function and phenotypic changes are compared with appropriate control animals such as genetically modified animals that receive placebo treatment, and/or animals with unaltered MBCAT expression that receive candidate therapeutic agent.

In addition to the above-described genetically modified animals having altered MBCAT function, animal models having defective beta-catenin function (and otherwise normal MBCAT function), can be used in the methods of the present invention. For example, a beta-catenin knockout mouse can be used to assess, *in vivo*, the activity of a candidate beta-catenin modulating agent identified in one of the *in vitro* assays described below. Preferably, the candidate beta-catenin modulating agent when administered to a model system with cells defective in beta-catenin function, produces a detectable phenotypic change in the model system indicating that the beta-catenin function is restored, i.e., the cells exhibit normal cell cycle progression.

Modulating Agents

The invention provides methods to identify agents that interact with and/or modulate the function of MBCAT and/or the beta-catenin pathway. Modulating agents identified by the methods are also part of the invention. Such agents are useful in a variety of diagnostic and therapeutic applications associated with the beta-catenin pathway, as well as in further analysis of the MBCAT protein and its contribution to the beta-catenin pathway. Accordingly, the invention also provides methods for modulating the beta-catenin pathway comprising the step of specifically modulating MBCAT activity by administering a MBCAT-interacting or -modulating agent.

As used herein, an "MBCAT-modulating agent" is any agent that modulates MBCAT function, for example, an agent that interacts with MBCAT to inhibit or enhance MBCAT activity or otherwise affect normal MBCAT function. MBCAT function can be affected at any level, including transcription, protein expression, protein localization, and

cellular or extra-cellular activity. In a preferred embodiment, the MBCAT - modulating agent specifically modulates the function of the MBCAT. The phrases "specific modulating agent", "specifically modulates", etc., are used herein to refer to modulating agents that directly bind to the MBCAT polypeptide or nucleic acid, and preferably inhibit, enhance, or otherwise alter, the function of the MBCAT. These phrases also encompass modulating agents that alter the interaction of the MBCAT with a binding partner, substrate, or cofactor (e.g. by binding to a binding partner of an MBCAT, or to a protein/binding partner complex, and altering MBCAT function). In a further preferred embodiment, the MBCAT- modulating agent is a modulator of the beta-catenin pathway (e.g. it restores and/or upregulates beta-catenin function) and thus is also a beta-catenin-modulating agent.

Preferred MBCAT-modulating agents include small molecule compounds; MBCAT-interacting proteins, including antibodies and other biotherapeutics; and nucleic acid modulators such as antisense and RNA inhibitors. The modulating agents may be formulated in pharmaceutical compositions, for example, as compositions that may comprise other active ingredients, as in combination therapy, and/or suitable carriers or excipients. Techniques for formulation and administration of the compounds may be found in "Remington's Pharmaceutical Sciences" Mack Publishing Co., Easton, PA, 19th edition.

Small molecule modulators

Small molecules are often preferred to modulate function of proteins with enzymatic function, and/or containing protein interaction domains. Chemical agents, referred to in the art as "small molecule" compounds are typically organic, non-peptide molecules, having a molecular weight less than 10,000, preferably less than 5,000, more preferably less than 1,000, and most preferably less than 500 daltons. This class of modulators includes chemically synthesized molecules, for instance, compounds from combinatorial chemical libraries. Synthetic compounds may be rationally designed or identified based on known or inferred properties of the MBCAT protein or may be identified by screening compound libraries. Alternative appropriate modulators of this class are natural products, particularly secondary metabolites from organisms such as plants or fungi, which can

also be identified by screening compound libraries for MBCAT–modulating activity. Methods for generating and obtaining compounds are well known in the art (Schreiber SL, Science (2000) 151: 1964-1969; Radmann J and Gunther J, Science (2000) 151:1947-1948).

Small molecule modulators identified from screening assays, as described below, can be used as lead compounds from which candidate clinical compounds may be designed, optimized, and synthesized. Such clinical compounds may have utility in treating pathologies associated with the beta-catenin pathway. The activity of candidate small molecule modulating agents may be improved several-fold through iterative secondary functional validation, as further described below, structure determination, and candidate modulator modification and testing. Additionally, candidate clinical compounds are generated with specific regard to clinical and pharmacological properties. For example, the reagents may be derivatized and re-screened using *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

Protein Modulators

Specific MBCAT-interacting proteins are useful in a variety of diagnostic and therapeutic applications related to the beta-catenin pathway and related disorders, as well as in validation assays for other MBCAT-modulating agents. In a preferred embodiment, MBCAT-interacting proteins affect normal MBCAT function, including transcription, protein expression, protein localization, and cellular or extra-cellular activity. In another embodiment, MBCAT-interacting proteins are useful in detecting and providing information about the function of MBCAT proteins, as is relevant to beta-catenin related disorders, such as cancer (e.g., for diagnostic means).

An MBCAT-interacting protein may be endogenous, i.e. one that naturally interacts genetically or biochemically with an MBCAT, such as a member of the MBCAT pathway that modulates MBCAT expression, localization, and/or activity. MBCAT-modulators include dominant negative forms of MBCAT-interacting proteins and of MBCAT proteins themselves. Yeast two-hybrid and variant screens offer preferred methods for identifying endogenous MBCAT-interacting proteins (Finley, R. L. et al. (1996) in DNA Cloning-Expression Systems: A Practical Approach, eds. Glover D. &

Hames B. D (Oxford University Press, Oxford, England), pp. 169-203; Fashema SF et al., Gene (2000) 250:1-14; Drees BL Curr Opin Chem Biol (1999) 3:64-70; Vidal M and Legrain P Nucleic Acids Res (1999) 27:919-29; and U.S. Pat. No. 5,928,868). Mass spectrometry is an alternative preferred method for the elucidation of protein complexes (reviewed in, e.g., Pandley A and Mann M, Nature (2000) 405:837-846; Yates JR 3rd, Trends Genet (2000) 16:5-8).

An MBCAT-interacting protein may be an exogenous protein, such as an MBCAT-specific antibody or a T-cell antigen receptor (see, e.g., Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory; Harlow and Lane (1999) Using antibodies: a laboratory manual. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press). MBCAT antibodies are further discussed below.

In preferred embodiments, an MBCAT-interacting protein specifically binds an MBCAT protein. In alternative preferred embodiments, an MBCAT-modulating agent binds an MBCAT substrate, binding partner, or cofactor.

Antibodies

In another embodiment, the protein modulator is an MBCAT specific antibody agonist or antagonist. The antibodies have therapeutic and diagnostic utilities, and can be used in screening assays to identify MBCAT modulators. The antibodies can also be used in dissecting the portions of the MBCAT pathway responsible for various cellular responses and in the general processing and maturation of the MBCAT.

Antibodies that specifically bind MBCAT polypeptides can be generated using known methods. Preferably the antibody is specific to a mammalian ortholog of MBCAT polypeptide, and more preferably, to human MBCAT. Antibodies may be polyclonal, monoclonal (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab').sub.2 fragments, fragments produced by a FAb expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Epitopes of MBCAT which are particularly antigenic can be selected, for example, by routine screening of MBCAT polypeptides for antigenicity or by applying a theoretical method for selecting antigenic regions of a protein (Hopp and Wood (1981), Proc. Nati. Acad. Sci. U.S.A. 78:3824-28; Hopp and Wood, (1983) Mol. Immunol. 20:483-89;

Sutcliffe et al., (1983) Science 219:660-66) to the amino acid sequence of an MBCAT. Monoclonal antibodies with affinities of 10^8 M^{-1} preferably 10^9 M^{-1} to 10^{10} M^{-1}, or stronger can be made by standard procedures as described (Harlow and Lane, *supra*; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed) Academic Press, New York; and U.S. Pat. Nos. 4,381,292; 4,451,570; and 4,618,577). Antibodies may be generated against crude cell extracts of MBCAT or substantially purified fragments thereof. If MBCAT fragments are used, they preferably comprise at least 10, and more preferably, at least 20 contiguous amino acids of an MBCAT protein. In a particular embodiment, MBCAT-specific antigens and/or immunogens are coupled to carrier proteins that stimulate the immune response. For example, the subject polypeptides are covalently coupled to the keyhole limpet hemocyanin (KLH) carrier, and the conjugate is emulsified in Freund's complete adjuvant, which enhances the immune response. An appropriate immune system such as a laboratory rabbit or mouse is immunized according to conventional protocols.

The presence of MBCAT-specific antibodies is assayed by an appropriate assay such as a solid phase enzyme-linked immunosorbant assay (ELISA) using immobilized corresponding MBCAT polypeptides. Other assays, such as radioimmunoassays or fluorescent assays might also be used.

Chimeric antibodies specific to MBCAT polypeptides can be made that contain different portions from different animal species. For instance, a human immunoglobulin constant region may be linked to a variable region of a murine mAb, such that the antibody derives its biological activity from the human antibody, and its binding specificity from the murine fragment. Chimeric antibodies are produced by splicing together genes that encode the appropriate regions from each species (Morrison et al., Proc. Natl. Acad. Sci. (1984) 81:6851-6855; Neuberger et al., Nature (1984) 312:604-608; Takeda et al., Nature (1985) 31:452-454). Humanized antibodies, which are a form of chimeric antibodies, can be generated by grafting complementary-determining regions (CDRs) (Carlos, T. M., J. M. Harlan. 1994. Blood 84:2068-2101) of mouse antibodies into a background of human framework regions and constant regions by recombinant DNA technology (Riechmann LM, et al., 1988 Nature 323: 323-327). Humanized antibodies contain ~10% murine sequences and ~90% human sequences, and thus further

reduce or eliminate immunogenicity, while retaining the antibody specificities (Co MS, and Queen C. 1991 Nature 351: 501-501; Morrison SL. 1992 Ann. Rev. Immun. 10:239-265). Humanized antibodies and methods of their production are well-known in the art (U.S. Pat. Nos. 5,530,101, 5,585,089, 5,693,762, and 6,180,370).

MBCAT-specific single chain antibodies which are recombinant, single chain polypeptides formed by linking the heavy and light chain fragments of the Fv regions via an amino acid bridge, can be produced by methods known in the art (U.S. Pat. No. 4,946,778; Bird, Science (1988) 242:423-426; Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85:5879-5883; and Ward et al., Nature (1989) 334:544-546).

Other suitable techniques for antibody production involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors (Huse et al., Science (1989) 246:1275-1281). As used herein, T-cell antigen receptors are included within the scope of antibody modulators (Harlow and Lane, 1988, *supra*).

The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, antibodies will be labeled by joining, either covalently or non-covalently, a substance that provides for a detectable signal, or that is toxic to cells that express the targeted protein (Menard S, et al., Int J. Biol Markers (1989) 4:131-134). A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, fluorescent emitting lanthanide metals, chemiluminescent moieties, bioluminescent moieties, magnetic particles, and the like (U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241). Also, recombinant immunoglobulins may be produced (U.S. Pat. No. 4,816,567). Antibodies to cytoplasmic polypeptides may be delivered and reach their targets by conjugation with membrane-penetrating toxin proteins (U.S. Pat. No. 6,086,900).

When used therapeutically in a patient, the antibodies of the subject invention are typically administered parenterally, when possible at the target site, or intravenously. The therapeutically effective dose and dosage regimen is determined by clinical studies. Typically, the amount of antibody administered is in the range of about 0.1 mg/kg –to

about 10 mg/kg of patient weight. For parenteral administration, the antibodies are formulated in a unit dosage injectable form (e.g., solution, suspension, emulsion) in association with a pharmaceutically acceptable vehicle. Such vehicles are inherently nontoxic and non-therapeutic. Examples are water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles such as fixed oils, ethyl oleate, or liposome carriers may also be used. The vehicle may contain minor amounts of additives, such as buffers and preservatives, which enhance isotonicity and chemical stability or otherwise enhance therapeutic potential. The antibodies' concentrations in such vehicles are typically in the range of about 1 mg/ml to about10 mg/ml. Immunotherapeutic methods are further described in the literature (US Pat. No. 5,859,206; WO0073469).

Specific biotherapeutics

In a preferred embodiment, an MBCAT-interacting protein may have biotherapeutic applications. Biotherapeutic agents formulated in pharmaceutically acceptable carriers and dosages may be used to activate or inhibit signal transduction pathways. This modulation may be accomplished by binding a ligand, thus inhibiting the activity of the pathway; or by binding a receptor, either to inhibit activation of, or to activate, the receptor. Alternatively, the biotherapeutic may itself be a ligand capable of activating or inhibiting a receptor. Biotherapeutic agents and methods of producing them are described in detail in U.S. Pat. No. 6,146,628.

When the MBCAT is a ligand, it may be used as a biotherapeutic agent to activate or inhibit its natural receptor. Alternatively, antibodies against MBCAT, as described in the previous section, may be used as biotherapeutic agents.

When the MBCAT is a receptor, its ligand(s), antibodies to the ligand(s) or the MBCAT itself may be used as biotherapeutics to modulate the activity of MBCAT in the beta-catenin pathway.

Nucleic Acid Modulators

Other preferred MBCAT-modulating agents comprise nucleic acid molecules, such as antisense oligomers or double stranded RNA (dsRNA), which generally inhibit MBCAT

activity. Preferred nucleic acid modulators interfere with the function of the MBCAT nucleic acid such as DNA replication, transcription, translocation of the MBCAT RNA to the site of protein translation, translation of protein from the MBCAT RNA, splicing of the MBCAT RNA to yield one or more mRNA species, or catalytic activity which may be engaged in or facilitated by the MBCAT RNA.

In one embodiment, the antisense oligomer is an oligonucleotide that is sufficiently complementary to an MBCAT mRNA to bind to and prevent translation, preferably by binding to the 5′ untranslated region. MBCAT-specific antisense oligonucleotides, preferably range from at least 6 to about 200 nucleotides. In some embodiments the oligonucleotide is preferably at least 10, 15, or 20 nucleotides in length. In other embodiments, the oligonucleotide is preferably less than 50, 40, or 30 nucleotides in length. The oligonucleotide can be DNA or RNA or a chimeric mixture or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents that facilitate transport across the cell membrane, hybridization-triggered cleavage agents, and intercalating agents.

In another embodiment, the antisense oligomer is a phosphothioate morpholino oligomer (PMO). PMOs are assembled from four different morpholino subunits, each of which contain one of four genetic bases (A, C, G, or T) linked to a six-membered morpholine ring. Polymers of these subunits are joined by non-ionic phosphodiamidate intersubunit linkages. Details of how to make and use PMOs and other antisense oligomers are well known in the art (e.g. see WO99/18193; Probst JC, Antisense Oligodeoxynucleotide and Ribozyme Design, Methods. (2000) 22(3):271-281; Summerton J, and Weller D. 1997 Antisense Nucleic Acid Drug Dev. :7:187-95; US Pat. No. 5,235,033; and US Pat No. 5,378,841).

Alternative preferred MBCAT nucleic acid modulators are double-stranded RNA species mediating RNA interference (RNAi). RNAi is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by double-stranded RNA (dsRNA) that is homologous in sequence to the silenced gene. Methods relating to the use of RNAi to silence genes in *C. elegans*, *Drosophila*, plants, and humans are

known in the art (Fire A, et al., 1998 Nature 391:806-811; Fire, A. Trends Genet. 15, 358-363 (1999); Sharp, P. A. RNA interference 2001. Genes Dev. 15, 485-490 (2001); Hammond, S. M., et al., Nature Rev. Genet. 2, 110-1119 (2001); Tuschl, T. Chem. Biochem. 2, 239-245 (2001); Hamilton, A. et al., Science 286, 950-952 (1999); Hammond, S. M., et al., Nature 404, 293-296 (2000); Zamore, P. D., et al., Cell 101, 25-33 (2000); Bernstein, E., et al., Nature 409, 363-366 (2001); Elbashir, S. M., et al., Genes Dev. 15, 188-200 (2001); WO0129058; WO9932619; Elbashir SM, et al., 2001 Nature 411:494-498).

Nucleic acid modulators are commonly used as research reagents, diagnostics, and therapeutics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used to elucidate the function of particular genes (see, for example, U.S. Pat. No. 6,165,790). Nucleic acid modulators are also used, for example, to distinguish between functions of various members of a biological pathway. For example, antisense oligomers have been employed as therapeutic moieties in the treatment of disease states in animals and man and have been demonstrated in numerous clinical trials to be safe and effective (Milligan JF, *et al*, Current Concepts in Antisense Drug Design, J Med Chem. (1993) 36:1923-1937; Tonkinson JL *et al.*, Antisense Oligodeoxynucleotides as Clinical Therapeutic Agents, Cancer Invest. (1996) 14:54-65). Accordingly, in one aspect of the invention, an MBCAT-specific nucleic acid modulator is used in an assay to further elucidate the role of the MBCAT in the beta-catenin pathway, and/or its relationship to other members of the pathway. In another aspect of the invention, an MBCAT-specific antisense oligomer is used as a therapeutic agent for treatment of beta-catenin-related disease states.

Assay Systems

The invention provides assay systems and screening methods for identifying specific modulators of MBCAT activity. As used herein, an "assay system" encompasses all the components required for performing and analyzing results of an assay that detects and/or measures a particular event. In general, primary assays are used to identify or confirm a modulator's specific biochemical or molecular effect with respect to the MBCAT nucleic acid or protein. In general, secondary assays further assess the activity of a MBCAT

modulating agent identified by a primary assay and may confirm that the modulating agent affects MBCAT in a manner relevant to the beta-catenin pathway. In some cases, MBCAT modulators will be directly tested in a secondary assay.

In a preferred embodiment, the screening method comprises contacting a suitable assay system comprising an MBCAT polypeptide or nucleic acid with a candidate agent under conditions whereby, but for the presence of the agent, the system provides a reference activity (e.g. kinase activity), which is based on the particular molecular event the screening method detects. A statistically significant difference between the agent-biased activity and the reference activity indicates that the candidate agent modulates MBCAT activity, and hence the beta-catenin pathway. The MBCAT polypeptide or nucleic acid used in the assay may comprise any of the nucleic acids or polypeptides described above.

Primary Assays

The type of modulator tested generally determines the type of primary assay.

Primary assays for small molecule modulators

For small molecule modulators, screening assays are used to identify candidate modulators. Screening assays may be cell-based or may use a cell-free system that recreates or retains the relevant biochemical reaction of the target protein (reviewed in Sittampalam GS *et al.*, Curr Opin Chem Biol (1997) 1:384-91 and accompanying references). As used herein the term "cell-based" refers to assays using live cells, dead cells, or a particular cellular fraction, such as a membrane, endoplasmic reticulum, or mitochondrial fraction. The term "cell free" encompasses assays using substantially purified protein (either endogenous or recombinantly produced), partially purified or crude cellular extracts. Screening assays may detect a variety of molecular events, including protein-DNA interactions, protein-protein interactions (*e.g.*, receptor-ligand binding), transcriptional activity (*e.g.*, using a reporter gene), enzymatic activity (*e.g.*, via a property of the substrate), activity of second messengers, immunogenicty and changes in cellular morphology or other cellular characteristics. Appropriate screening assays may use a wide range of detection methods including fluorescent, radioactive,

colorimetric, spectrophotometric, and amperometric methods, to provide a read-out for the particular molecular event detected.

Cell-based screening assays usually require systems for recombinant expression of MBCAT and any auxiliary proteins demanded by the particular assay. Appropriate methods for generating recombinant proteins produce sufficient quantities of proteins that retain their relevant biological activities and are of sufficient purity to optimize activity and assure assay reproducibility. Yeast two-hybrid and variant screens, and mass spectrometry provide preferred methods for determining protein-protein interactions and elucidation of protein complexes. In certain applications, when MBCAT-interacting proteins are used in screens to identify small molecule modulators, the binding specificity of the interacting protein to the MBCAT protein may be assayed by various known methods such as substrate processing (e.g. ability of the candidate MBCAT-specific binding agents to function as negative effectors in MBCAT-expressing cells), binding equilibrium constants (usually at least about $10^7 M^{-1}$, preferably at least about $10^8 M^{-1}$, more preferably at least about $10^9 M^{-1}$), and immunogenicity (e.g. ability to elicit MBCAT specific antibody in a heterologous host such as a mouse, rat, goat or rabbit). For enzymes and receptors, binding may be assayed by, respectively, substrate and ligand processing.

The screening assay may measure a candidate agent's ability to specifically bind to or modulate activity of a MBCAT polypeptide, a fusion protein thereof, or to cells or membranes bearing the polypeptide or fusion protein. The MBCAT polypeptide can be full length or a fragment thereof that retains functional MBCAT activity. The MBCAT polypeptide may be fused to another polypeptide, such as a peptide tag for detection or anchoring, or to another tag. The MBCAT polypeptide is preferably human MBCAT, or is an ortholog or derivative thereof as described above. In a preferred embodiment, the screening assay detects candidate agent-based modulation of MBCAT interaction with a binding target, such as an endogenous or exogenous protein or other substrate that has MBCAT –specific binding activity, and can be used to assess normal MBCAT gene function.

Suitable assay formats that may be adapted to screen for MBCAT modulators are known in the art. Preferred screening assays are high throughput or ultra high throughput

and thus provide automated, cost-effective means of screening compound libraries for lead compounds (Fernandes PB, Curr Opin Chem Biol (1998) 2:597-603; Sundberg SA, Curr Opin Biotechnol 2000, 11:47-53). In one preferred embodiment, screening assays uses fluorescence technologies, including fluorescence polarization, time-resolved fluorescence, and fluorescence resonance energy transfer. These systems offer means to monitor protein-protein or DNA-protein interactions in which the intensity of the signal emitted from dye-labeled molecules depends upon their interactions with partner molecules (*e.g.*, Selvin PR, Nat Struct Biol (2000) 7:730-4; Fernandes PB, *supra*; Hertzberg RP and Pope AJ, Curr Opin Chem Biol (2000) 4:445-451).

A variety of suitable assay systems may be used to identify candidate MBCAT and beta-catenin pathway modulators (e.g. U.S. Pat. No. 6,165,992 (kinase assays); U.S. Pat. Nos. 5,550,019 and 6,133,437 (apoptosis assays); and U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434 (angiogenesis assays), among others). Specific preferred assays are described in more detail below.

Protein kinases, key signal transduction proteins that may be either membrane-associated or intracellular, catalyze the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. Radioassays, which monitor the transfer from [gamma-^{32}P or -^{33}P]ATP, are frequently used to assay kinase activity. For instance, a scintillation assay for p56 (lck) kinase activity monitors the transfer of the gamma phosphate from [gamma -^{33}P] ATP to a biotinylated peptide substrate. The substrate is captured on a streptavidin coated bead that transmits the signal (Beveridge M *et al.*, J Biomol Screen (2000) 5:205-212). This assay uses the scintillation proximity assay (SPA), in which only radio-ligand bound to receptors tethered to the surface of an SPA bead are detected by the scintillant immobilized within it, allowing binding to be measured without separation of bound from free ligand. Other assays for protein kinase activity may use antibodies that specifically recognize phosphorylated substrates. For instance, the kinase receptor activation (KIRA) assay measures receptor tyrosine kinase activity by ligand stimulating the intact receptor in cultured cells, then capturing solubilized receptor with specific antibodies and quantifying phosphorylation via phosphotyrosine ELISA (Sadick MD, Dev Biol Stand (1999) 97:121-133). Another example of antibody based assays for protein kinase

activity is TRF (time-resolved fluorometry). This method utilizes europium chelate-labeled anti-phosphotyrosine antibodies to detect phosphate transfer to a polymeric substrate coated onto microtiter plate wells. The amount of phosphorylation is then detected using time-resolved, dissociation-enhanced fluorescence (Braunwalder AF, et al., Anal Biochem 1996 Jul 1;238(2):159-64).

Transporter proteins carry a range of substrates, including nutrients, ions, amino acids, and drugs, across cell membranes. Assays for modulators of transporters may use labeled substrates. For instance, exemplary high throughput screens to identify compounds that interact with different peptide and anion transporters both use fluorescently labeled substrates; the assay for peptide transport additionally uses multiscreen filtration plates (Blevitt JM et al., J Biomol Screen 1999, 4:87-91; Cihlar T and Ho ES, Anal Biochem 2000, 283:49-55).

Ion channels mediate essential physiological functions, including fluid secretion, electrolyte balance, bioenergetics, and membrane excitability. Assays for channel activity can incorporate ion-sensitive dyes or proteins or voltage-sensitive dyes or proteins, as reviewed in Gonzalez JE *et al.* (Drug Discovery Today (1999) 4:431-439). Alternative methods measure the displacement of known ligands, which may be radio-labeled or fluorescently labeled (*e.g.*, ScHMid EL *et al.*, Anal Chem (1998) 70:1331-1338).

Transcription factors control gene transcription. Electrophoretic mobility shift assay (EMSA) or gel shift assay is one of the most powerful methods for studying protein-DNA interactions. High throughput gel shift assays for transcription factors may involve fluorescence (Cyano dye Cy5) labeled oligodeoxynucleotide duplexes as specific probes and an automatic DNA sequencer for analysis (Ruscher K, et al., (2000) J Biotechnol 78:163-70). Alternatively high throughput methods involve colorimetric assays (Renard P, et al. (2001) Nucleic Acids Res 29(4):E21), or homogeneous fluorescence assays for the detection and quantification of sequence-specific DNA-binding proteins (Heyduk T, and Heyduk E (2001) Nat Biotechnol 20:171-6.)

High throughput assays based on photometric analysis of the activity of decarboxylase enzymes have been described (Breuer M et al (2002) Anal Bioanal Chem 374:1069-73).

High-throughput photometric assays for peroxidases have been described (Smith AD et al (2001) Int J Vitam Nutr Res 71:87-92; Smith AD and Levander OA (2002) Methods Enzymol 347:113-21).

High throughput adenylyl cyclase assays are known in the art, and are also commercially available (NEN® Adenylyl Cyclase Activation FlashPlate® Assay, available from Perkin Elmer Life Sciences, Boston, MA). Examples include homogeneous cellular assays that allow direct measurement of receptor-mediated adenylyl cyclase activation/inhibition.

Apoptosis assays. Assays for apoptosis may be performed by terminal deoxynucleotidyl transferase-mediated digoxigenin-11-dUTP nick end labeling (TUNEL) assay. The TUNEL assay is used to measure nuclear DNA fragmentation characteristic of apoptosis (Lazebnik *et al.*, 1994, Nature 371, 346), by following the incorporation of fluorescein-dUTP (Yonehara *et al.*, 1989, J. Exp. Med. 169, 1747). Apoptosis may further be assayed by acridine orange staining of tissue culture cells (Lucas, R., et al., 1998, Blood 15:4730-41). Other cell-based apoptosis assays include the caspase-3/7 assay and the cell death nucleosome ELISA assay. The caspase 3/7 assay is based on the activation of the caspase cleavage activity as part of a cascade of events that occur during programmed cell death in many apoptotic pathways. In the caspase 3/7 assay (commercially available Apo-ONE™ Homogeneous Caspase-3/7 assay from Promega, cat# 67790), lysis buffer and caspase substrate are mixed and added to cells. The caspase substrate becomes fluorescent when cleaved by active caspase 3/7. The nucleosome ELISA assay is a general cell death assay known to those skilled in the art, and available commercially (Roche, Cat# 1774425). This assay is a quantitative sandwich-enzyme-immunoassay which uses monoclonal antibodies directed against DNA and histones respectively, thus specifically determining amount of mono- and oligonucleosomes in the cytoplasmic fraction of cell lysates. Mono and oligonucleosomes are enriched in the cytoplasm during apoptosis due to the fact that DNA fragmentation occurs several hours before the plasma membrane breaks down, allowing for accumalation in the cytoplasm. Nucleosomes are not present in the cytoplasmic fraction of cells that are not undergoing apoptosis. An apoptosis assay system may comprise a cell that expresses an MBCAT,

and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the apoptosis assay system and changes in induction of apoptosis relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, an apoptosis assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using a cell-free assay system. An apoptosis assay may also be used to test whether MBCAT function plays a direct role in apoptosis. For example, an apoptosis assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in apoptotic response compared to wild type cells suggests that the MBCAT plays a direct role in the apoptotic response. Apoptosis assays are described further in US Pat. No. 6,133,437.

Cell proliferation and cell cycle assays. Cell proliferation may be assayed via bromodeoxyuridine (BRDU) incorporation. This assay identifies a cell population undergoing DNA synthesis by incorporation of BRDU into newly-synthesized DNA. Newly-synthesized DNA may then be detected using an anti-BRDU antibody (Hoshino *et al.*, 1986, Int. J. Cancer 38, 369; Campana *et al.*, 1988, J. Immunol. Meth. 107, 79), or by other means.

Cell proliferation is also assayed via phospho-histone H3 staining, which identifies a cell population undergoing mitosis by phosphorylation of histone H3. Phosphorylation of histone H3 at serine 10 is detected using an antibody specfic to the phosphorylated form of the serine 10 residue of histone H3. (Chadlee,D.N. 1995, J. Biol. Chem 270:20098-105). Cell Proliferation may also be examined using [^{3}H]-thymidine incorporation (Chen, J., 1996, Oncogene 13:1395-403; Jeoung, J., 1995, J. Biol. Chem. 270:18367-73). This assay allows for quantitative characterization of S-phase DNA syntheses. In this assay, cells synthesizing DNA will incorporate [^{3}H]-thymidine into newly synthesized DNA. Incorporation can then be measured by standard techniques such as by counting of radioisotope in a scintillation counter (e.g., Beckman LS 3800 Liquid Scintillation Counter). Another proliferation assay uses the dye Alamar Blue (available from Biosource International), which fluoresces when reduced in living cells and provides an

indirect measurement of cell number (Voytik-Harbin SL et al., 1998, In Vitro Cell Dev Biol Anim 34:239-46). Yet another proliferation assay, the MTS assay, is based on in vitro cytotoxicity assessment of industrial chemicals, and uses the soluble tetrazolium salt, MTS. MTS assays are commercially available, for example, the Promega CellTiter 96® AQueous Non-Radioactive Cell Proliferation Assay (Cat.# G5421).

Cell proliferation may also be assayed by colony formation in soft agar (Sambrook et al., Molecular Cloning, Cold Spring Harbor (1989)). For example, cells transformed with MBCAT are seeded in soft agar plates, and colonies are measured and counted after two weeks incubation.

Cell proliferation may also be assayed by measuring ATP levels as indicator of metabolically active cells. Such assays are commercially available, for example Cell Titer-Glo™, which is a luminescent homogeneous assay available from Promega.

Involvement of a gene in the cell cycle may be assayed by flow cytometry (Gray JW et al. (1986) Int J Radiat Biol Relat Stud Phys Chem Med 49:237-55). Cells transfected with an MBCAT may be stained with propidium iodide and evaluated in a flow cytometer (available from Becton Dickinson), which indicates accumulation of cells in different stages of the cell cycle.

Accordingly, a cell proliferation or cell cycle assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the assay system and changes in cell proliferation or cell cycle relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, the cell proliferation or cell cycle assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system such as a cell-free assay system. A cell proliferation assay may also be used to test whether MBCAT function plays a direct role in cell proliferation or cell cycle. For example, a cell proliferation or cell cycle assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in proliferation or cell cycle compared to wild type cells suggests that the MBCAT plays a direct role in cell proliferation or cell cycle.

Angiogenesis. Angiogenesis may be assayed using various human endothelial cell systems, such as umbilical vein, coronary artery, or dermal cells. Suitable assays include Alamar Blue based assays (available from Biosource International) to measure proliferation; migration assays using fluorescent molecules, such as the use of Becton Dickinson Falcon HTS FluoroBlock cell culture inserts to measure migration of cells through membranes in presence or absence of angiogenesis enhancer or suppressors; and tubule formation assays based on the formation of tubular structures by endothelial cells on Matrigel® (Becton Dickinson). Accordingly, an angiogenesis assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the angiogenesis assay system and changes in angiogenesis relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, the angiogenesis assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system. An angiogenesis assay may also be used to test whether MBCAT function plays a direct role in cell proliferation. For example, an angiogenesis assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in angiogenesis compared to wild type cells suggests that the MBCAT plays a direct role in angiogenesis. U.S. Pat. Nos. 5,976,782, 6,225,118 and 6,444,434, among others, describe various angiogenesis assays.

Hypoxic induction. The alpha subunit of the transcription factor, hypoxia inducible factor-1 (HIF-1), is upregulated in tumor cells following exposure to hypoxia in vitro. Under hypoxic conditions, HIF-1 stimulates the expression of genes known to be important in tumour cell survival, such as those encoding glyolytic enzymes and VEGF. Induction of such genes by hypoxic conditions may be assayed by growing cells transfected with MBCAT in hypoxic conditions (such as with 0.1% O2, 5% CO2, and balance N2, generated in a Napco 7001 incubator (Precision Scientific)) and normoxic conditions, followed by assessment of gene activity or expression by Taqman®. For example, a hypoxic induction assay system may comprise a cell that expresses an MBCAT, and that optionally has defective beta-catenin function (e.g. beta-catenin is

over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the hypoxic induction assay system and changes in hypoxic response relative to controls where no test agent is added, identify candidate beta-catenin modulating agents. In some embodiments of the invention, the hypoxic induction assay may be used as a secondary assay to test a candidate beta-catenin modulating agents that is initially identified using another assay system. A hypoxic induction assay may also be used to test whether MBCAT function plays a direct role in the hypoxic response. For example, a hypoxic induction assay may be performed on cells that over- or under-express MBCAT relative to wild type cells. Differences in hypoxic response compared to wild type cells suggests that the MBCAT plays a direct role in hypoxic induction.

Cell adhesion. Cell adhesion assays measure adhesion of cells to purified adhesion proteins, or adhesion of cells to each other, in presence or absence of candidate modulating agents. Cell-protein adhesion assays measure the ability of agents to modulate the adhesion of cells to purified proteins. For example, recombinant proteins are produced, diluted to 2.5g/mL in PBS, and used to coat the wells of a microtiter plate. The wells used for negative control are not coated. Coated wells are then washed, blocked with 1% BSA, and washed again. Compounds are diluted to 2× final test concentration and added to the blocked, coated wells. Cells are then added to the wells, and the unbound cells are washed off. Retained cells are labeled directly on the plate by adding a membrane-permeable fluorescent dye, such as calcein-AM, and the signal is quantified in a fluorescent microplate reader.

Cell-cell adhesion assays measure the ability of agents to modulate binding of cell adhesion proteins with their native ligands. These assays use cells that naturally or recombinantly express the adhesion protein of choice. In an exemplary assay, cells expressing the cell adhesion protein are plated in wells of a multiwell plate. Cells expressing the ligand are labeled with a membrane-permeable fluorescent dye, such as BCECF , and allowed to adhere to the monolayers in the presence of candidate agents. Unbound cells are washed off, and bound cells are detected using a fluorescence plate reader.

High-throughput cell adhesion assays have also been described. In one such assay, small molecule ligands and peptides are bound to the surface of microscope slides using a microarray spotter, intact cells are then contacted with the slides, and unbound cells are washed off. In this assay, not only the binding specificity of the peptides and modulators against cell lines are determined, but also the functional cell signaling of attached cells using immunofluorescence techniques in situ on the microchip is measured (Falsey JR et al., Bioconjug Chem. 2001 May-Jun;12(3):346-53).

Tubulogenesis. Tubulogenesis assays monitor the ability of cultured cells, generally endothelial cells, to form tubular structures on a matrix substrate, which generally simulates the environment of the extracellular matrix. Exemplary substrates include Matrigel™ (Becton Dickinson), an extract of basement membrane proteins containing laminin, collagen IV, and heparin sulfate proteoglycan, which is liquid at 4° C and forms a solid gel at 37° C. Other suitable matrices comprise extracellular components such as collagen, fibronectin, and/or fibrin. Cells are stimulated with a pro-angiogenic stimulant, and their ability to form tubules is detected by imaging. Tubules can generally be detected after an overnight incubation with stimuli, but longer or shorter time frames may also be used. Tube formation assays are well known in the art (e.g., Jones MK et al., 1999, Nature Medicine 5:1418-1423). These assays have traditionally involved stimulation with serum or with the growth factors FGF or VEGF. Serum represents an undefined source of growth factors. In a preferred embodiment, the assay is performed with cells cultured in serum free medium, in order to control which process or pathway a candidate agent modulates. Moreover, we have found that different target genes respond differently to stimulation with different pro-angiogenic agents, including inflammatory angiogenic factors such as TNF-alpa. Thus, in a further preferred embodiment, a tubulogenesis assay system comprises testing an MBCAT's response to a variety of factors, such as FGF, VEGF, phorbol myristate acetate (PMA), TNF-alpha, ephrin, etc.

Cell Migration. An invasion/migration assay (also called a migration assay) tests the ability of cells to overcome a physical barrier and to migrate towards pro-angiogenic

signals. Migration assays are known in the art (e.g., Paik JH et al., 2001, J Biol Chem 276:11830-11837). In a typical experimental set-up, cultured endothelial cells are seeded onto a matrix-coated porous lamina, with pore sizes generally smaller than typical cell size. The matrix generally simulates the environment of the extracellular matrix, as described above. The lamina is typically a membrane, such as the transwell polycarbonate membrane (Corning Costar Corporation, Cambridge, MA), and is generally part of an upper chamber that is in fluid contact with a lower chamber containing pro-angiogenic stimuli. Migration is generally assayed after an overnight incubation with stimuli, but longer or shorter time frames may also be used. Migration is assessed as the number of cells that crossed the lamina, and may be detected by staining cells with hemotoxylin solution (VWR Scientific, South San Francisco, CA), or by any other method for determining cell number. In another exemplary set up, cells are fluorescently labeled and migration is detected using fluorescent readings, for instance using the Falcon HTS FluoroBlok (Becton Dickinson). While some migration is observed in the absence of stimulus, migration is greatly increased in response to pro-angiogenic factors. As described above, a preferred assay system for migration/invasion assays comprises testing an MBCAT's response to a variety of pro-angiogenic factors, including tumor angiogenic and inflammatory angiogenic agents, and culturing the cells in serum free medium.

Sprouting assay. A sprouting assay is a three-dimensional *in vitro* angiogenesis assay that uses a cell-number defined spheroid aggregation of endothelial cells ("spheroid"), embedded in a collagen gel-based matrix. The spheroid can serve as a starting point for the sprouting of capillary-like structures by invasion into the extracellular matrix (termed "cell sprouting") and the subsequent formation of complex anastomosing networks (Korff and Augustin, 1999, J Cell Sci 112:3249-58). In an exemplary experimental set-up, spheroids are prepared by pipetting 400 human umbilical vein endothelial cells into individual wells of a nonadhesive 96-well plates to allow overnight spheroidal aggregation (Korff and Augustin: J Cell Biol 143: 1341-52, 1998). Spheroids are harvested and seeded in 900μl of methocel-collagen solution and pipetted into individual wells of a 24 well plate to allow collagen gel polymerization. Test agents

are added after 30 min by pipetting 100 μl of 10-fold concentrated working dilution of the test substances on top of the gel. Plates are incubated at 37°C for 24h. Dishes are fixed at the end of the experimental incubation period by addition of paraformaldehyde. Sprouting intensity of endothelial cells can be quantitated by an automated image analysis system to determine the cumulative sprout length per spheroid.

Primary assays for antibody modulators

For antibody modulators, appropriate primary assays test is a binding assay that tests the antibody's affinity to and specificity for the MBCAT protein. Methods for testing antibody affinity and specificity are well known in the art (Harlow and Lane, 1988, 1999, *supra*). The enzyme-linked immunosorbant assay (ELISA) is a preferred method for detecting MBCAT-specific antibodies; others include FACS assays, radioimmunoassays, and fluorescent assays.

In some cases, screening assays described for small molecule modulators may also be used to test antibody modulators.

Primary assays for nucleic acid modulators

For nucleic acid modulators, primary assays may test the ability of the nucleic acid modulator to inhibit or enhance MBCAT gene expression, preferably mRNA expression. In general, expression analysis comprises comparing MBCAT expression in like populations of cells (*e.g.*, two pools of cells that endogenously or recombinantly express MBCAT) in the presence and absence of the nucleic acid modulator. Methods for analyzing mRNA and protein expression are well known in the art. For instance, Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR (*e.g.*, using the TaqMan®, PE Applied Biosystems), or microarray analysis may be used to confirm that MBCAT mRNA expression is reduced in cells treated with the nucleic acid modulator (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, *eds.*, John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm DH and Guiseppi-Elie, A Curr Opin Biotechnol 2001, 12:41-47). Protein expression may also be monitored. Proteins are most commonly detected with specific antibodies or antisera directed against either

the MBCAT protein or specific peptides. A variety of means including Western blotting, ELISA, or in situ detection, are available (Harlow E and Lane D, 1988 and 1999, *supra*).

In some cases, screening assays described for small molecule modulators, particularly in assay systems that involve MBCAT mRNA expression, may also be used to test nucleic acid modulators.

Secondary Assays

Secondary assays may be used to further assess the activity of MBCAT-modulating agent identified by any of the above methods to confirm that the modulating agent affects MBCAT in a manner relevant to the beta-catenin pathway. As used herein, MBCAT-modulating agents encompass candidate clinical compounds or other agents derived from previously identified modulating agent. Secondary assays can also be used to test the activity of a modulating agent on a particular genetic or biochemical pathway or to test the specificity of the modulating agent's interaction with MBCAT.

Secondary assays generally compare like populations of cells or animals (*e.g.*, two pools of cells or animals that endogenously or recombinantly express MBCAT) in the presence and absence of the candidate modulator. In general, such assays test whether treatment of cells or animals with a candidate MBCAT–modulating agent results in changes in the beta-catenin pathway in comparison to untreated (or mock- or placebo-treated) cells or animals. Certain assays use "sensitized genetic backgrounds", which, as used herein, describe cells or animals engineered for altered expression of genes in the beta-catenin or interacting pathways.

Cell-based assays

Cell based assays may detect endogenous beta-catenin pathway activity or may rely on recombinant expression of beta-catenin pathway components. Any of the aforementioned assays may be used in this cell-based format. Candidate modulators are typically added to the cell media but may also be injected into cells or delivered by any other efficacious means.

Animal Assays

A variety of non-human animal models of normal or defective beta-catenin pathway may be used to test candidate MBCAT modulators. Models for defective beta-catenin pathway typically use genetically modified animals that have been engineered to mis-express (*e.g.*, over-express or lack expression in) genes involved in the beta-catenin pathway. Assays generally require systemic delivery of the candidate modulators, such as by oral administration, injection, etc.

In a preferred embodiment, beta-catenin pathway activity is assessed by monitoring neovascularization and angiogenesis. Animal models with defective and normal beta-catenin are used to test the candidate modulator's affect on MBCAT in Matrigel® assays. Matrigel® is an extract of basement membrane proteins, and is composed primarily of laminin, collagen IV, and heparin sulfate proteoglycan. It is provided as a sterile liquid at 4^{o} C, but rapidly forms a solid gel at 37^{o} C. Liquid Matrigel® is mixed with various angiogenic agents, such as bFGF and VEGF, or with human tumor cells which over-express the MBCAT. The mixture is then injected subcutaneously(SC) into female athymic nude mice (Taconic, Germantown, NY) to support an intense vascular response. Mice with Matrigel® pellets may be dosed via oral (PO), intraperitoneal (IP), or intravenous (IV) routes with the candidate modulator. Mice are euthanized 5 - 12 days post-injection, and the Matrigel® pellet is harvested for hemoglobin analysis (Sigma plasma hemoglobin kit). Hemoglobin content of the gel is found to correlate the degree of neovascularization in the gel.

In another preferred embodiment, the effect of the candidate modulator on MBCAT is assessed via tumorigenicity assays. Tumor xenograft assays are known in the art (see, e.g., Ogawa K et al., 2000, Oncogene 19:6043-6052). Xenografts are typically implanted SC into female athymic mice, 6-7 week old, as single cell suspensions either from a pre-existing tumor or from *in vitro* culture. The tumors which express the MBCAT endogenously are injected in the flank, 1×10^5 to 1×10^7 cells per mouse in a volume of 100 µL using a 27gauge needle. Mice are then ear tagged and tumors are measured twice weekly. Candidate modulator treatment is initiated on the day the mean tumor weight reaches 100 mg. Candidate modulator is delivered IV, SC, IP, or PO by bolus administration. Depending upon the pharmacokinetics of each unique candidate modulator, dosing can be performed multiple times per day. The tumor weight is

assessed by measuring perpendicular diameters with a caliper and calculated by multiplying the measurements of diameters in two dimensions. At the end of the experiment, the excised tumors maybe utilized for biomarker identification or further analyses. For immunohistochemistry staining, xenograft tumors are fixed in 4% paraformaldehyde, 0.1M phosphate, pH 7.2, for 6 hours at 4°C, immersed in 30% sucrose in PBS, and rapidly frozen in isopentane cooled with liquid nitrogen.

In another preferred embodiment, tumorogenicity is monitored using a hollow fiber assay, which is described in U.S. Pat No. US 5,698,413. Briefly, the method comprises implanting into a laboratory animal a biocompatible, semi-permeable encapsulation device containing target cells, treating the laboratory animal with a candidate modulating agent, and evaluating the target cells for reaction to the candidate modulator. Implanted cells are generally human cells from a pre-existing tumor or a tumor cell line. After an appropriate period of time, generally around six days, the implanted samples are harvested for evaluation of the candidate modulator. Tumorogenicity and modulator efficacy may be evaluated by assaying the quantity of viable cells present in the macrocapsule, which can be determined by tests known in the art, for example, MTT dye conversion assay, neutral red dye uptake, trypan blue staining, viable cell counts, the number of colonies formed in soft agar, the capacity of the cells to recover and replicate in vitro, etc.

In another preferred embodiment, a tumorogenicity assay use a transgenic animal, usually a mouse, carrying a dominant oncogene or tumor suppressor gene knockout under the control of tissue specific regulatory sequences; these assays are generally referred to as transgenic tumor assays. In a preferred application, tumor development in the transgenic model is well characterized or is controlled. In an exemplary model, the "RIP1-Tag2" transgene, comprising the SV40 large T-antigen oncogene under control of the insulin gene regulatory regions is expressed in pancreatic beta cells and results in islet cell carcinomas (Hanahan D, 1985, Nature 315:115-122; Parangi S et al, 1996, Proc Natl Acad Sci USA 93: 2002-2007; Bergers G et al, 1999, Science 284:808-812). An "angiogenic switch," occurs at approximately five weeks, as normally quiescent capillaries in a subset of hyperproliferative islets become angiogenic. The RIP1-TAG2 mice die by age 14 weeks. Candidate modulators may be administered

at a variety of stages, including just prior to the angiogenic switch (e.g., for a model of tumor prevention), during the growth of small tumors (e.g., for a model of intervention), or during the growth of large and/or invasive tumors (e.g., for a model of regression). Tumorogenicity and modulator efficacy can be evaluating life-span extension and/or tumor characteristics, including number of tumors, tumor size, tumor morphology, vessel density, apoptotic index, etc.

Diagnostic and therapeutic uses

Specific MBCAT-modulating agents are useful in a variety of diagnostic and therapeutic applications where disease or disease prognosis is related to defects in the beta-catenin pathway, such as angiogenic, apoptotic, or cell proliferation disorders. Accordingly, the invention also provides methods for modulating the beta-catenin pathway in a cell, preferably a cell pre-determined to have defective or impaired beta-catenin function (e.g. due to overexpression, underexpression, or misexpression of beta-catenin, or due to gene mutations), comprising the step of administering an agent to the cell that specifically modulates MBCAT activity. Preferably, the modulating agent produces a detectable phenotypic change in the cell indicating that the beta-catenin function is restored. The phrase "function is restored", and equivalents, as used herein, means that the desired phenotype is achieved, or is brought closer to normal compared to untreated cells. For example, with restored beta-catenin function, cell proliferation and/or progression through cell cycle may normalize, or be brought closer to normal relative to untreated cells. The invention also provides methods for treating disorders or disease associated with impaired beta-catenin function by administering a therapeutically effective amount of an MBCAT -modulating agent that modulates the beta-catenin pathway. The invention further provides methods for modulating MBCAT function in a cell, preferably a cell pre-determined to have defective or impaired MBCAT function, by administering an MBCAT -modulating agent. Additionally, the invention provides a method for treating disorders or disease associated with impaired MBCAT function by administering a therapeutically effective amount of an MBCAT -modulating agent.

The discovery that MBCAT is implicated in beta-catenin pathway provides for a variety of methods that can be employed for the diagnostic and prognostic evaluation of

diseases and disorders involving defects in the beta-catenin pathway and for the identification of subjects having a predisposition to such diseases and disorders.

Various expression analysis methods can be used to diagnose whether MBCAT expression occurs in a particular sample, including Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR, and microarray analysis. (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, *eds.*, John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm and Guiseppi-Elie, Curr Opin Biotechnol 2001, 12:41-47). Tissues having a disease or disorder implicating defective beta-catenin signaling that express an MBCAT, are identified as amenable to treatment with an MBCAT modulating agent. In a preferred application, the beta-catenin defective tissue overexpresses an MBCAT relative to normal tissue. For example, a Northern blot analysis of mRNA from tumor and normal cell lines, or from tumor and matching normal tissue samples from the same patient, using full or partial MBCAT cDNA sequences as probes, can determine whether particular tumors express or overexpress MBCAT. Alternatively, the TaqMan® is used for quantitative RT-PCR analysis of MBCAT expression in cell lines, normal tissues and tumor samples (PE Applied Biosystems).

Various other diagnostic methods may be performed, for example, utilizing reagents such as the MBCAT oligonucleotides, and antibodies directed against an MBCAT, as described above for: (1) the detection of the presence of MBCAT gene mutations, or the detection of either over- or under-expression of MBCAT mRNA relative to the non-disorder state; (2) the detection of either an over- or an under-abundance of MBCAT gene product relative to the non-disorder state; and (3) the detection of perturbations or abnormalities in the signal transduction pathway mediated by MBCAT.

Thus, in a specific embodiment, the invention is drawn to a method for diagnosing a disease or disorder in a patient that is associated with alterations in MBCAT expression, the method comprising: a) obtaining a biological sample from the patient; b) contacting the sample with a probe for MBCAT expression; c) comparing results from step (b) with a control; and d) determining whether step (c) indicates a likelihood of the disease or disorder. Preferably, the disease is cancer. The probe may be either DNA or protein, including an antibody.

EXAMPLES

The following experimental section and examples are offered by way of illustration and not by way of limitation.

I. Drosophila beta-catenin screen

Two dominant loss of function screens were carried out in *Drosophila* to identify genes that interact with the Wg cell signaling molecule, beta –catenin (Riggleman et al. (1990) Cell 63:549-560; Peifer et al. (1991) Development 111:1029-1043). Late stage activation of the pathway in the developing *Drosophila* eye leads to apoptosis (Freeman and Bienz (2001) EMBO reports 2: 157-162), whereas early stage activation leads to an overgrowth phenotype. We discovered that ectopic expression of the activated protein in the wing results in changes of cell fate into ectopic bristles and wing veins.

Each transgene was carried in a separate fly stock:

Stocks and genotypes were as follows:

eye overgrowth transgene: isow; P{3.5 eyeless-Gal4}; P{arm(S56F)-pExp-UAS)}/TM6b;

eye apoptosis transgene: y w; P{arm(S56F)-pExp-GMR}/CyO; and

wing transgene: P{arm(ΔN)-pExp-VgMQ}/FM7c

In the first dominant loss of function screen, females of each of these three transgenes were crossed to a collection of males containing genomic deficiencies. Resulting progeny containing the transgene and the deficiency were then scored for the effect of the deficiency on the eye apoptosis, eye overgrowth, and wing phenotypes, i.e., whether the deficiency enhanced, suppressed, or had no effect on their respective phenotypes. All data was recorded and all modifiers were retested with a repeat of the original cross. Modifying deficiencies of the phenotypes were then prioritized according to how they modified each of the three phenotypes.

Transposons contained within the prioritized deficiencies were then screened as described. Females of each of the three transgenes were crossed to a collection of 4 types of transposons (3 piggyBac-based and 1 P-element-based). The resulting progeny containing the transgene and the transposon were scored for the effect of the transposon

on their respective phenotypes. All data was recorded and all modifiers were retested with a repeat of the original cross. Modifiers of the phenotypes were identified as either members of the Wg pathway, components of apoptotic related pathways, components of cell cycle related pathways, or cell adhesion related proteins.

In the second dominant loss of function screen, females of the eye overgrowth transgene were crossed to males from a collection of 3 types of piggyBac-based transposons. The resulting progeny containing the transgene and the transposon were scored for the effect of the transposon on the eye overgrowth phenotype. All data was recorded and all modifiers were retested with a repeat of the original cross. Modifiers of the phenotypes were identified as either members of the Wg pathway, components of cell cycle related pathways, or cell adhesion related proteins.

II. Analysis of Table 1

BLAST analysis (Altschul et al., *supra*) was employed to identify orthologs of *Drosophila* modifiers. The columns "MBCAT symbol", and "MBCAT name aliases " provide a symbol and the known name abbreviations for the Targets, where available, from Genbank. "MBCAT RefSeq_NA or GI_NA", "MBCAT GI_AA", "MBCAT NAME", and "MBCAT Description" provide the reference DNA sequences for the MBCATs as available from National Center for Biology Information (NCBI), MBCAT protein Genbank identifier number (GI#), MBCAT name, and MBCAT description, all available from Genbank, respectively. The length of each amino acid is in the "MBCAT Protein Length" column.

Names and Protein sequences of *Drosophila* modifiers of beta-catenin from screen (Example I), are represented in the "Modifier Name" and "Modifier GI_AA" column by GI#, respectively.

Table 1

MBCAT symbol	MBCAT name aliases	MBCAT RefSeq_NA or GI_NA	MBCAT GI_AA	MBCAT name	MBCAT description	MBCAT protein length	Modifier name	Modifier gi_aa

ADCY5	ADCY5 | adenylate cyclase 5 | adenylyl cyclase type V | adenylyl cyclase type 5	XM_171048	22212711	adenylate cyclase 5	response to hypoxia	894	CG32158	24665354
ADCY6	KIAA0422 | adenylate cyclase 6 | ADCY6 | adenylyl cyclase type VI	NM_015270|NM_020983	10181096	adenylate cyclase 6	regulation of smooth muscle contraction; cAMP biosynthesis	1168	CG32158	24665354
ADCY8	ADCY8 | ADCY3 | HBAC1 | Adenylyl cyclase-8, brain | adenylate cyclase 8 (brain) | adenylyl cyclase type VIII	NM_001115	4557257	adenylate cyclase 8 (brain)	learning and/or memory; response to drug; signal transduction	1251	CG32158	24665354
CENTG1	CENTG1 | PIKE | AGAP2 | GGAP2 | KIAA0167 | centaurin gamma1 | phosphoinositide 3-kinase enhancer | GTP-binding and GTPase activating protein 2 | Arf GAP with GTP-binding protein-like, ANK repeat and PH domains 2 | centaurin, gamma 1	NM_014770|NM_023017	7661962	centaurin, gamma 1	na	836	cenG1A	24584217
CENTG2	CENTG2 | AGAP1 | GGAP1 | KIAA1099 | GTP-binding and GTPase-activating protein 1 | Arf GAP with GTP-binding protein-like, ANK repeat and PH domains 1 | centaurin, gamma 2	NM_014914	7662484	centaurin, gamma 2	vesicle-mediated transport; actin cytoskeleton organization and biogenesis	804	cenG1A	24584217
CENTG3	CENTG3 | MRIP-1 | MRIP-1 protein | centaurin, gamma 3	NM_031946	16799069	centaurin, gamma 3	cell growth and/or maintenance; signal transduction; signal transduction	875	cenG1A	24584217

DDX17	DDX17 | P72 | RH70 | probable RNA-dependent helicase p72 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17 (72kD) | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 17, 72kDa | DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	NM_006386|NM_030881	5453840	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	regulation of transcription from Pol II promoter; RNA processing	650	Rm62	24644481
DDX5	DDX5 | P68 | HLR1 | G17P1 | HUMP68 | RNA-dependent ATPase | DEAD/H box-5 (RNA helicase, 68kD) | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kDa) | p68 | DEAD box-5 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	NM_004396	4758138	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	mRNA splicing	614	Rm62	24644481
FLJ10665	FLJ10665 | hypothetical protein FLJ10665	NM_018173	8922581	hypothetical protein FLJ10665	Rho protein signal transduction; cell growth and/or maintenance	790	CG7323	7293694
KIAA0720	KIAA0720 | KIAA0720 protein	XM_030970	29728516	KIAA0720 protein	Rho protein signal transduction; cell growth and/or maintenance	1083	CG7323	7293694
FLJ20530	FLJ20530 | hypothetical protein FLJ20530	NM_017864	8923496	hypothetical protein FLJ20530	na	557	EG:EG0003.5	18484916

GABRA2	GABRA2 | gamma-aminobutyric acid (GABA) A receptor, alpha 2	NM_000807	4557601	gamma-aminobutyric acid (GABA) A receptor, alpha 2	gamma-amino butyric acid signaling pathway; gamma-amino butyric acid signaling pathway; chloride transport; regulation of neurotransmitter levels	451	GluClalpha	24648249
GABRA5	GABRA5 | gamma-aminobutyric acid (GABA) A receptor, alpha 5	NM_000810	4503861	gamma-aminobutyric acid (GABA) A receptor, alpha 5	gamma-amino butyric acid signaling pathway; chloride transport; synaptic transmission; signal transduction	462	GluClalpha	24648249
GLRA1	GLRA1 | STHE | glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome)	NM_000171	4504019	glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome)	cell surface receptor linked signal transduction; neurogenesis; chloride transport; chloride transport; synaptic transmission; synaptic transmission; synaptic transmission	449	GluClalpha	24648249
GYG	GYG | glycogenin	NM_004130	20127457	glycogenin	glycogen biosynthesis; glycogen biosynthesis; glycogen biosynthesis	350	Glycogenin	24656813
GYG2	GYG2 | GN2 | GN-2 | glycogenin 2	NM_003918	5453674	glycogenin 2	glycogen biosynthesis; glycogen biosynthesis	501	Glycogenin	24656813
LOC350705	LOC350705 | similar to Glycogenin-1	XM_301113	30147855	similar to Glycogenin-1	na	233	Glycogenin	24656813

MLLT10	MLLT10 | AF10 | ALL1 fused gene from chromosome 10 | myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	NM_004641	4757726	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	na	1027	Alhambra	24644741
MLLT6	MLLT6 | AF17 | Myeloid/lymphoid or mixed-lineage leukemia, translocated to, 6 | myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 6 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	NM_005937	5174577	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	cell growth and/or maintenance; regulation of transcription, DNA-dependent	1093	Alhambra	24644741
POU2F1	POU2F1 | OCT1 | OTF1 | Octamer-binding transcription factor-1 | POU domain, class 2, transcription factor 1	NM_002697	4505957	POU domain, class 2, transcription factor 1	transcription from Pol II promoter; regulation of transcription from Pol II promoter; negative regulation of transcription; regulation of transcription from Pol III promoter	743	pdm2	24583942
POU2F2	POU2F2 | OCT2 | OTF2 | POU domain, class 2, transcription factor 2	NM_002698	4505959	POU domain, class 2, transcription factor 2	transcription from Pol II promoter; regulation of transcription, DNA-dependent; humoral immune response; membrane fusion; pathogenesis; development	463	pdm2	24583942

POU2F3	POU2F3 | OCT11 | PLA-1 | Epoc-1 | Skn-1a | POU transcription factor | likely ortholog of mouse POU domain, class 2, transcription factor 3 | POU domain, class 2, transcription factor 3	NM_014352	7657409	POU domain, class 2, transcription factor 3	keratinocyte differentiation; epidermal differentiation; regulation of transcription from Pol II promoter	436	pdm2	24583942
PRKCI	PKCI | DXS1179E | protein kinase C, iota | PRKCI | PKCi	NM_002740	4506071	protein kinase C, iota	anti-apoptosis; signal transduction; signal transduction; protein amino acid phosphorylation	587	aPKC	24653760

PRKCZ	protein kinase C, zeta | PRKCZ | PKC2 | PKCz | zeta protein kinase C | protein kinase C zeta | PKC zeta	NM_002744	10864650	protein kinase C, zeta	insulin receptor signaling pathway; cytokinesis; glucose transport; antibacterial humoral response (sensu Vertebrata); activation of MAP/ERK kinase kinase; positive regulation of transcription from Pol II promoter; actin cytoskeleton organization and biogenesis; T-cell activation; protein kinase cascade; anti-apoptosis; chemotaxis; positive regulation of cell proliferation; monocyte activation; cytokine biosynthesis; cytokine and chemokine mediated signaling pathway; cell cycle arrest; signal transduction; signal transduction; signal transduction; inflammatory response; protein amino acid phosphorylation; protein amino acid phosphorylation; protein amino acid phosphorylation; protein amino acid phosphorylation	592	aPKC	24653760

SLC1A2	SLC1A2 | EAAT2 | GLT-1 | glutamate/aspartate transporter II | excitatory amino acid transporter 2 | H.sapiens mRNA for glutamate transporter | glial high affinity glutamate transporter | solute carrier family 1 (glial high affinity glutamate transporter), member 2	NM_004171	4759124	solute carrier family 1 (glial high affinity glutamate transporter), member 2	neurotransmitter uptake; synaptic transmission; glutamate transport; glutamate transport	574	Eaat2	17137666
SLC1A3	SLC1A3 | EAAT1 | GLAST | GLAST1 | solute carrier family 1 (glial high affinity glutamate transporter), member 3	NM_004172	4759126	solute carrier family 1 (glial high affinity glutamate transporter), member 3	neurotransmitter uptake; neurotransmitter uptake; neurotransmitter uptake; synaptic transmission; glutamate transport; glutamate transport	542	Eaat2	17137666
SLC1A7	SLC1A7 | AAAT | EAAT5 | excitatory amino acid transporter 5 (retinal glutamate transporter) | solute carrier family 1 (glutamate transporter), member 7	NM_006671	20070239	solute carrier family 1 (glutamate transporter), member 7	vision; glutamate transport	560	Eaat2	17137666
SLC1A4	SLC1A4 | SATT | ASCT1 | glutamate/neutral amino acid transporter | alanine/serine/cysteine/threonine transporter | solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	NM_003038	21314632	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	neutral amino acid transport; neutral amino acid transport	532	Eaat2	17137666

SLC1A6	SLC1A6 | EAAT4 | excitatory amino acid transporter 4 | solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	NM_005071	4827012	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	aspartate transport; chloride transport; synaptic transmission; glutamate transport; glutamate transport; glutamate transport	564	Eaat2	17137666
SLC1A1	SLC1A1 | EAAC1 | EAAT3 | excitatory amino acid carrier 1 | excitatory amino acid transporter-3 | solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	NM_004170	18252049	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	synaptic transmission; glutamate transport	524	Eaat2	17137666
SLC1A5	SLC1A5 | R16 | AAAT | ATBO | M7V1 | RDRC | ASCT2 | M7VS1 | RD114 virus receptor | baboon M7 virus receptor | neutral amino acid transporter B | solute carrier family 1 (neutral amino acid transporter), member 5	NM_005628	5032093	solute carrier family 1 (neutral amino acid transporter), member 5	neutral amino acid transport; neutral amino acid transport; EGF receptor signaling pathway	541	Eaat2	17137666
SLC7A1	SLC7A1 | ERR | ATRC1 | CAT-1 | HCAT1 | REC1L | ecotropic retroviral receptor | amino acid transporter, cationic 1 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	NM_003045	4507047	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	basic amino acid transport; amino acid transport; arginine transport; amino acid metabolism	629	CG11128	7296600

SLC7A2	SLC7A2 | ATRC2 | CAT-2 | HCAT2 | amino acid transporter, cationic 2 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	NM_003046	4507049	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	basic amino acid transport; amino acid metabolism	657	CG11128	7296600
SLC7A3	SLC7A3 | ATRC3 | CAT-3 | FLJ14541 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	NM_032803	17939406	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	amino acid transport; amino acid transport; amino acid metabolism; L-amino acid transport; L-amino acid transport	619	CG11128	7296600
SULF2	SULF2 | SULF-2 | HSULF-2 | KIAA1247 | sulfatase 2 | similar to glucosamine-6-sulfatases	NM_018837|XM_030036	29789100	similar to glucosamine-6-sulfatases	metabolism	870	Sulf1	18487383
SULF1	SULF1 | SULF-1 | HSULF-1 | KIAA1077 | sulfatase FP | sulfatase 1	NM_015170	29789064	sulfatase 1	metabolism	871	Sulf1	18487383
LOC151531	LOC151531 | liver-specific uridine phosphorylase	NM_173355	27597096	liver-specific uridine phosphorylase	na	317	CG6330	23172399
UP	UP | uridine phosphorylase	NM_003364|NM_181597	4507839	uridine phosphorylase	nucleobase, nucleoside, nucleotide and nucleic acid metabolism; response to drug; response to drug; response to drug; response to drug	310	CG6330	23172399

RAB32	RAB32 | RAB32, member RAS oncogene family	NM_006834	5803133	RAB32, member RAS oncogene family	small GTPase mediated signal transduction; organelle organization and biogenesis; protein-vacuolar targeting; exocytosis; endocytosis; mitochondrial membrane organization and biogenesis; membrane fusion	225	Rab-RP1	6561893
RAB38	RAB38 | NY-MEL-1 | Rab-related GTP-binding protein | RAB38, member RAS oncogene family	NM_022337	11641237	RAB38, member RAS oncogene family	small GTPase mediated signal transduction; vesicle-mediated transport	211	Rab-RP1	6561893
RAB7L1	RAB7L1 | RAB7, member RAS oncogene family-like 1	NM_003929	4506375	RAB7, member RAS oncogene family-like 1	na	203	Rab-RP1	6561893
C6orf37	C6orf37 | FLJ20037 | retinal expressed gene C6orf37 | chromosome 6 open reading frame 37	NM_017633	8923042	chromosome 6 open reading frame 37	na	447	CG30497	24586361
FLJ20202	FLJ20202 | hypothetical protein FLJ20202	NM_017709	8923192	hypothetical protein FLJ20202	na	391	CG30497	24586361
MGC16491	MGC16491 | MGC20845 | hypothetical protein MGC16491	NM_052943	16418427	hypothetical protein MGC16491	na	424	CG30497	24586361
MGC26999	MGC26999 | hypothetical protein MGC26999	NM_152630	22749287	hypothetical protein MGC26999	na	389	CG30497	24586361

III. <u>High-Throughput In Vitro Fluorescence Polarization Assay</u>

Fluorescently-labeled MBCAT peptide/substrate are added to each well of a 96-well microtiter plate, along with a test agent in a test buffer (10 mM HEPES, 10 mM NaCl, 6 mM magnesium chloride, pH 7.6). Changes in fluorescence polarization, determined by using a Fluorolite FPM-2 Fluorescence Polarization Microtiter System (Dynatech Laboratories, Inc), relative to control values indicates the test compound is a candidate modifier of MBCAT activity.

IV. <u>High-Throughput In Vitro Binding Assay.</u>

^{33}P-labeled MBCAT peptide is added in an assay buffer (100 mM KCl, 20 mM HEPES pH 7.6, 1 mM $MgCl_2$, 1% glycerol, 0.5% NP-40, 50 mM beta-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors) along with a test agent to the wells of a Neutralite-avidin coated assay plate and incubated at 25°C for 1 hour. Biotinylated substrate is then added to each well and incubated for 1 hour. Reactions are stopped by washing with PBS, and counted in a scintillation counter. Test agents that cause a difference in activity relative to control without test agent are identified as candidate beta-catenin modulating agents.

V. <u>Immunoprecipitations and Immunoblotting</u>

For coprecipitation of transfected proteins, 3×10^6 appropriate recombinant cells containing the MBCAT proteins are plated on 10-cm dishes and transfected on the following day with expression constructs. The total amount of DNA is kept constant in each transfection by adding empty vector. After 24 h, cells are collected, washed once with phosphate-buffered saline and lysed for 20 min on ice in 1 ml of lysis buffer containing 50 mM Hepes, pH 7.9, 250 mM NaCl, 20 mM -glycerophosphate, 1 mM sodium orthovanadate, 5 mM p-nitrophenyl phosphate, 2 mM dithiothreitol, protease inhibitors (complete, Roche Molecular Biochemicals), and 1% Nonidet P-40. Cellular debris is removed by centrifugation twice at $15,000 \times g$ for 15 min. The cell lysate is incubated with 25 μl of M2 beads (Sigma) for 2 h at 4 °C with gentle rocking.

After extensive washing with lysis buffer, proteins bound to the beads are solubilized by boiling in SDS sample buffer, fractionated by SDS-polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membrane and blotted with the indicated antibodies. The reactive bands are visualized with horseradish peroxidase coupled to the appropriate secondary antibodies and the enhanced chemiluminescence (ECL) Western blotting detection system (Amersham Pharmacia Biotech).

VI. Kinase assay

A purified or partially purified MBCAT is diluted in a suitable reaction buffer, e.g., 50 mM Hepes, pH 7.5, containing magnesium chloride or manganese chloride (1-20 mM) and a peptide or polypeptide substrate, such as myelin basic protein or casein (1-10 μg/ml). The final concentration of the kinase is 1-20 nM. The enzyme reaction is conducted in microtiter plates to facilitate optimization of reaction conditions by increasing assay throughput. A 96-well microtiter plate is employed using a final volume 30-100 μl. The reaction is initiated by the addition of ^{33}P-gamma-ATP (0.5 μCi/ml) and incubated for 0.5 to 3 hours at room temperature. Negative controls are provided by the addition of EDTA, which chelates the divalent cation ($Mg2^{+}$ or Mn^{2+}) required for enzymatic activity. Following the incubation, the enzyme reaction is quenched using EDTA. Samples of the reaction are transferred to a 96-well glass fiber filter plate (MultiScreen, Millipore). The filters are subsequently washed with phosphate-buffered saline, dilute phosphoric acid (0.5%) or other suitable medium to remove excess radiolabeled ATP. Scintillation cocktail is added to the filter plate and the incorporated radioactivity is quantitated by scintillation counting (Wallac/Perkin Elmer). Activity is defined by the amount of radioactivity detected following subtraction of the negative control reaction value (EDTA quench).

VII. Expression analysis

All cell lines used in the following experiments are NCI (National Cancer Institute) lines, and are available from ATCC (American Type Culture Collection, Manassas, VA 20110-2209). Normal and tumor tissues are obtained from Impath, UC Davis, Clontech, Stratagene, Ardais, Genome Collaborative, and Ambion.

TaqMan analysis is used to assess expression levels of the disclosed genes in various samples.

RNA is extracted from each tissue sample using Qiagen (Valencia, CA) RNeasy kits, following manufacturer's protocols, to a final concentration of 50ng/μl. Single stranded cDNA is then synthesized by reverse transcribing the RNA samples using random hexamers and 500ng of total RNA per reaction, following protocol 4304965 of Applied Biosystems (Foster City, CA).

Primers for expression analysis using TaqMan assay (Applied Biosystems, Foster City, CA) are prepared according to the TaqMan protocols, and the following criteria: a) primer pairs are designed to span introns to eliminate genomic contamination, and b) each primer pair produced only one product. Expression analysis is performed using a 7900HT instrument.

Taqman reactions are carried out following manufacturer's protocols, in 25 μl total volume for 96-well plates and 10 μl total volume for 384-well plates, using 300nM primer and 250 nM probe, and approximately 25ng of cDNA. The standard curve for result analysis is prepared using a universal pool of human cDNA samples, which is a mixture of cDNAs from a wide variety of tissues so that the chance that a target will be present in appreciable amounts is good. The raw data are normalized using 18S rRNA (universally expressed in all tissues and cells).

For each expression analysis, tumor tissue samples are compared with matched normal tissues from the same patient. A gene is considered overexpressed in a tumor when the level of expression of the gene is 2 fold or higher in the tumor compared with its matched normal sample. In cases where normal tissue is not available, a universal pool of cDNA samples is used instead. In these cases, a gene is considered overexpressed in a tumor sample when the difference of expression levels between a tumor sample and the average of all normal samples from the same tissue type is greater than 2 times the standard deviation of all normal samples (i.e., Tumor – average(all normal samples) > 2 x STDEV(all normal samples)).

A modulator identified by an assay described herein can be further validated for therapeutic effect by administration to a tumor in which the gene is overexpressed. A decrease in tumor growth confirms therapeutic utility of the modulator. Prior to treating

a patient with the modulator, the likelihood that the patient will respond to treatment can be diagnosed by obtaining a tumor sample from the patient, and assaying for expression of the gene targeted by the modulator. The expression data for the gene(s) can also be used as a diagnostic marker for disease progression. The assay can be performed by expression analysis as described above, by antibody directed to the gene target, or by any other available detection method.

Nucleic Acid and Polypeptide sequences

>gi|27480832|ref|XM_171048.2| Homo sapiens adenylate cyclase 5 (ADCY5), mRNA
ACATCGTGGGTGTCTGCACCCACTATCCGGCTGAGGTCTCCCAGAGACAGGCTTTCCAGGAGACCCGAGA
GTGCATCCAGGCGCGGCTCCACTCGCAGCGGGAGAACCAGCAGCAGGAACGGCTCCTGCTGTCTGTCCTT
CCCCGTCATGTTGCCATGGAGATGAAAGCAGACATCAACGCCAAGCAGGAGGATATGATGTTCCATAAGA
TTTACATCCAGAAACATGACAACGTGAGCATCCTGTTTGCTGACATCGAGGGCTGAGGGGCCTCCGACTC
AGCTGGGGGTAGACGGGCTCGAATGTGGCCTGGGAGAGCCTAGGGGGCCCCAGGGGTCTGCTTTTCTATG
TGAGCCTTTAAACTTCAGACAGGCCACCACCCTGCACCTGCAGGGGCTTTGGCACAGGAGTGCTGGCTTT
GGAGGGACTGTGGCCTTCATCGTGGTCCTCTGCCCACACCTCCACGCACACAGACAGTGCCCTAGGAGGG
AAACAGAACTAATTACGAGGGGGAGGCAAGAGGACGCCAAGCAAGGAGTGGTGATTCTGAGAAAAATATT
TATTAAATAAAACAAAACAAGTTCTCCGTGCCCTTCTTTAGACTATGCTAGTTGTATGCGTGTAAGAGAC
ACACAAGCAAACGAGGACGCCACTCGGGGGGAGGGCGGGGATCCCCACTTGTCTTTTTGTATTTTTAT
TTTGTATTATTGAAAGCCTTGGAGATCTCACAGATAGATATGCCAAATTCTATATTTGTAAATTCTCTA
TATTAGAAAACAGCTGTGCACAGCAGGGCGGGTGTGCTCATTTGTACTGTGTGTATGTCGGTGTATGTAC
TGGTGTATATGTGTGTGTGTTCATGCTGTGGAACTGGTCTCACACAGGATGTGTTTCCCTCATTTCAGAT
TTGGCAGTTTTGGGTTTTCCAAGGTACCACCAGAGCAGTGGGTGTGTGCTTTTGGGGTACCATATGCTCA
GATTAAGTAGGAGGATGCATGGACACACTGCCCCATCTTTTCTGACACACGCACACGTATGTACACACAT
GCACACACCCTCCTTCCCCTAAGCAAAACGCAGATGGAATAAGAAAACAAAAAGCTGCTTTCCCATCCCA
GGCCGAGCTGGAACCAAGGGAAGCAATCTCATCCTGCGACAGGCAGTGTGGTGCCCTCCACACCCTGAGA
TTTCAGACGTTTGCGGCTTACAGAGGCAGCGCCCACAGATTCCAGAGTGCTTACAGAAGGCCAGGTGCTT
TGCAGGCTGGGACGAGGAAGCCAAGCCTCCCTGGCCTACTCAGTTGGCCAAGGTGCAGGTGGCTCTTCCT
GGAGATGTTCACTCAGACTGGGGGATGCAATGTGCAGCCTTCAGGTTTGCGGAAAGGGAGTGGCCTTGAC
CTCCACCGGCAAACCAGGCAGAGGAATGGGTAGAGCCCAGCTTTAGAGTCCACAGGGAAAGCTAGCAGGA
ATTTTGTTTTAGTGGGAGGGGGCAGTTAAACATACCAAGAAAAAAATACTATTTTTATAACCTATGAGGA
AGACATTTGGAAAATGATACTCTAGCACAGAATTCAGTGGAATCCTTAGGGCCCATGCCCAAATCTTTCC
ATTGCTTCTCAGGTTAGAATGATCTTCACCTCCAACATGAGCTTGGAGGTGATGAGGCAGTGGCTCTGTG
CCAGCTGCCACAATGTGACTTTGATGTCCACCTGTACCACCTCTCACTGGGCTCTAGCACCACCCTCCCC
TCCCCGCACACCAACTGAACACAGCTCTGAGAAGCAAAGTGTGTGGACCCAAAACTGCCAAGCCTGAGTC
TGTCCCGTGCTTCTGCTGCTCCATCCTTTGAGTTCTGCATTGCCATCCTGACGTCGGCCACAGGAGGCCT
GCTTTCTTCCAGCTGTTGTTCTCAAGTTCCCTGCCCCTCCACATCGCCCGCCAGTGGTGTTGGGTTTTCG
TTCTGCTTCCAACCTGAGTAAAGTGTGTGTGCTGAGTTCATCCCATGTTCTCCCATGGTCATGGCTTCCC
GGCCCCATGGGGACCCCTCTCCCATCCCAGCAGTGACTGGTGACAGTGTGCAGGTGCAGTGCTAGCTCTT
CGTTCCCTCTAAAGGGTGTGCACTCTTTTTATTCCTACTCTTGCAAAAACAGATACGATTATGATTTCCC
ATGGAAATTGAAAAGTCTATTTAAATAATTTAACTATTAAACACTTTCACTGGT

>gi|10947059|ref|NM_015270.2| Homo sapiens adenylate cyclase 6 (ADCY6), transcript variant 1, mRNA
CCGGTCTATAGGTGCATACCACCACACCAGGCTAATTTTTTTTTTTTGAGACGGAGTCTCACTCTGTCAC
CCAGGCTGGAGTGCAATGGCGCGATCTTTGCTCACTGCAACCTCTGCCACCCGGGTTCAAGCAATTCTCC
TGCCTCAGCTCCTGAGTAGCTGGGATTACAGGCGCCCGCCACCACGCCCGGCTAATTTTTGTATTTTTAG
TAGAGACGAGGTTTCACCATCTTGGCCAGGCTGGTCTTGAACTCCTGACCTTGTGATCTACCTGCCAGGG
CCTTCCAAAGTGCTGGGATTACGGACGTGAGCCACCACGCCTGGCCCAGGCTAATTTTTTGAAATTTTAA
TAGAGGCAGGGTCTTGCTGTATTGCCCAGGCTGCTCTCACATTCCTAGCCTTAAGCCATCCTCCTATCTC
GGCCTCACAAAGTGCTGGGATTACAGGTGTAAGCCACTGTGCCTGGTTTTGGGCAAGTTTCTTGTCCTGA
CTGTGTCTTGGGTTCTCACCTGTTGATTGGGGATACCCTTGTTGCCTACCTCCAAGTAATTTTATGAGGA
TGAAACTCATAGCTTGTCAGTGGGAAGTGCTTAGGTAATGAGCTACTAGTGGTGGCAGTGGCTGTGATGG
TGGTATTAATACCACTCCTACTGGATGGTCTCTAATACTATCTCCTTCCTTCCCTACCAGCAACATGTCA
TGGTTTAGTGGCCTCCTGGTCCCTAAAGTGGATGAACGGAAAACAGCCTGGGGCGAACGCAATGGGCAGA
AGCGTTCGCGGCGCCGTGGCACTCGGGCAGGTGGCTTCTGCACGCCCCGCTATATGAGCTGCCTCCGGGA
TGCAGAGCCACCCAGCCCCACCCCTGCCGGCCCCCCTCGGTGCCCCTGGCAGGATGACGCCTTCATCCGG
AGGGGCGGCCCAGGCAAGGGCAAGGAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCGAGGATACCGAGG
TGACAACGACAGCGGGCGGGACGGCTGAGGTGGCGCCCGACGCGGTGCCCAGGAGTGGGCGATCCTGCTG
GCGCCGTCTGGTGCAGGTGTTCCAGTCGAAGCAGTTCCGTTCGGCCAAGCTGGAGCGCCTGTACCAGCGG
TACTTCTTCCAGATGAACCAGAGCAGCCTGACGCTGCTGATGGCGGTGCTGGTGCTGCTCACAGCGGTGC
TGCTGGCTTTCCACGCCGCACCCGCCCGCCCTCAGCCTGCCTATGTGGCACTGTTGGCCTGTGCCGCCGC

CCTGTTCGTGGGGCTCATGGTGGTGTGTAACCGGCATAGCTTCCGCCAGGACTCCATGTGGGTGGTGAGC
TACGTGGTGCTGGGCATCCTGGCGGCAGTGCAGGTCGGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCCT
CTGCGGGCCTCTGGTGCCCTGTGTTCTTTGTCTACATCGCCTACACGCTCCTCCCCATCCGCATGCGGGC
TGCCGTCCTCAGCGGCCTGGGCCTCTCCACCTTGCATTTGATCTTGGCCTGGCAACTTAACCGTGGTGAT
GCCTTCCTCTGGAAGCAGCTCGGTGCCAATGTGCTGCTGTTCCTCTGCACCAACGTCATTGGCATCTGCA
CACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCCTTTCAGGAGACCCGCGGTTACATCCAGGCCCGGCT
CCACCTGCAGCATGAGAATCGGCAGCAGGAGCGGCTGCTGCTGTCGGTATTGCCCCAGCACGTTGCCATG
GAGATGAAAGAAGACATCAACACAAAAAAAGAAGACATGATGTTCCACAAGATCTACATACAGAAGCATG
ACAATGTCAGCATCCTGTTTGCAGACATTGAGGGCTTCACCAGCCTGGCATCCCAGTGCACTGCGCAGGA
GCTGGTCATGACCCTGAATGAGCTCTTTGCCCGGTTTGACAAGCTGGCTGCGGAGAATCACTGCCTGAGG
ATCAAGATCTTGGGGGACTGTTACTACTGTGTGTCAGGGCTGCCGGAGGCCCGGGCCGACCATGCCCACT
GCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTGAATGT
GAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCACTGCGGCGTCCTTGGCTTGCGGAAATGGCAGTTC
GATGTGTGGTCCAATGATGTGACCCTGGCCAACCACATGGAGGCAGGAGGCCGGGCTGGCCGCATCCACA
TCACTCGGGCAACACTGCAGTACCTGAACGGGGACTACGAGGTGGAGCCAGGCCGTGGTGGCGAGCGCAA
CGCGTACCTCAAGGAGCAGCACATTGAGACTTTCCTCATCCTGGGCGCCAGCCAGAAACGGAAAGAGGAG
AAGGCCATGCTGGCCAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCGCGCTGGGTTC
CTGATCGTGCCTTCTCCCGGACCAAGGACTCCAAGGCCTTCCGCCAGATGGGCATTGATGATTCCAGCAA
AGACAACCGGGGCACCCAAGATGCCCTGAACCCTGAGGATGAGGTGGATGAGTTCCTGAGCCGTGCCATC
GATGCCCGCAGCATTGATCAGCTGCGGAAGGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGG
ATCTTGAGAAGAAGTACTCCCGGAAGGTGGATCCCCGCTTCGGAGCCTACGTTGCCTGTGCCCTGTTGGT
CTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACACTCCACCCTGATGCTTGGGATCTATGCC
AGCATCTTCCTGCTGCTGCTAATCACCGTGCTGATCTGTGCTGTGTACTCCTGTGGTTCTCTGTTCCCTA
AGGCCCTGCAACGTCTGTCCCGCAGCATTGTCCGCTCACGGGCACATAGCACCGCAGTTGGCATCTTTTC
CGTCCTGCTTGTGTTTACTTCTGCCATTGCCAACATGTTCACCTGTAACCACACCCCCATACGGAGCTGT
GCAGCCCGGATGCTGAATTTAACACCTGCTGACATCACTGCCTGCCACCTGCAGCAGCTCAATTACTCTC
TGGGCCTGGATGCTCCCCTGTGTGAGGGCACCATGCCCACCTGCAGCTTTCCTGAGTACTTCATCGGGAA
CATGCTGCTGAGTCTCTTGGCCAGCTCTGTCTTCCTGCACATCAGCAGCATCGGGAAGTTGGCCATGATC
TTTGTCTTGGGGCTCATCTATTTGGTGCTGCTTCTGCTGGGTCCCCCAGCCACCATCTTTGACAACTATG
ACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGGCTGGACTGTCCAGCTGC
AGGGAGGGTGGCCCTCAAATATATGACCCCTGTGATTCTGCTGGTGTTTGCGCTGGCGCTGTATCTGCAT
GCTCAGCAGGTGGAGTCGACTGCCCGCCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAAGGAGG
AGATGGAGGAGCTACAGGCATACAACCGGAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCA
CTTCCTGGCCCGGGAGCGCCGCAATGATGAACTCTACTATCAGTCGTGTGAGTGTGTGGCTGTTATGTTT
GCCTCCATTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAACAATGAGGGTGTCGAGTGCCTGC
GGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGGAGCGGTTCCGGCAGCTGGAAAA
GATCAAGACGATTGGTAGCACCTACATGGCTGCCTCAGGGCTGAACGCCAGCACCTACGATCAGGTGGGC
CGCTCCCACATCACTGCCCTGGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGCACATCAATGAGC
ACTCCTTCAACAATTTCCAGATGAAGATTGGGCTGAACATGGGCCCAGTCGTGGCAGGTGTCATCGGGGC
TCGGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCACGGGGGTC
CCCGACCGAATCCAGGTGACCACGGACCTGTACCAGGTTCTAGCTGCCAAGGGCTACCAGCTGGAGTGTC
GAGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACCTACTTCCTCAATGGGGGCCCCAGCAGTTA
ACAGGGCCCAGCCACAAATTCAGCTGAAGGGACCAAGGTGGGCATTGAGTGGACTCTGTGCTCACTGGGT
GGAGCTGTGGCAGGGGGCACTGAGCCTCCAGACCCTGCTAACCACAAAAGGGAACATCCCAGCAGGCTGT
GCTTGGATCATGCTCGTCTGCCCTCAAGCTGGAAAACAAGGGGCTACCTACCGAGAGGATTATGCAAGTG
ACTTTCTTTCTTACTTGGGGTAGGGCTGTTCCCTCTCCAATCTTCCAGCCTTTGGGAGCAGGGGAGGGGT
CAGTAGCAGAAGCAGAGGGAGGCCTCTTGCCTGAGGGATTAAAATGGCAGCTTGCCATGCCTACCCTTCC
CTGTCTGTCTGGGCAGCAGGTTCAGGGCTGAGCCCTTCTTTTCCCTCTTTTTTCCTGGGAATATTTTGTA
CAATATTTTGTACAAAGACAGGCATGAGGAGTGCCTATTCCATGCTTGCCTTTGCAATACCTGCATCCCC
AGCACTGGTCCTGGGCACTTCCCCACCCCAGCCAGGTGTCCCTCCTATGCACAGAGCAGAGGAGGGAGAA
GCTCTGGGGAGCCAGCTTTGGCCATATTTCAGGAGAATGTTTCCATGTGCCAAATCTTAGTCCCATGATC
TGTCCCCAAAGGGGAACAAAGGGACCTCTGACAGCTTAGATTTAGCCCCAGTTCCTGCACGCTCCAGGGA
ACGGGGTGTCTGGCCTCACTGGTACTGTGAAAAATGCTCAGAGAGCAAGCCTGTGTGTGGGGATGTCAGG
TCAGGAGCTGGAAGTTCACCTGCAGGTGCCAAAGAGCAGGCCGGCCAGGGCTGGGGCAGTGCCAGACTCT
GATCTGAGGACCCCGTCGGGGTCCAGATCAGGTCACTCTGCCCCAGTGCTCTCTTGCTGTCTGCTGACAA
GGGGGCATGGAGCATCTCTTCCTCTTCTGTTGCCAAATAGAAAAGGGTCAGGGCATGGAGAAAGGTGACC
CTGATCCCAAACCTGCCCTCCCAAGTCTCTGGTGTTGGGGAGGGCCCGTGTGTTTGTGTAACTGTGTGTG

CATGTTGGTCTTTGTGTGCATATCTGTTTTCCAGGTCTATGTGAGTCCTTGTGCTCCTGCTCCTCAGCTC
TCCACCCCAGGTTGCCTCTCTCCTGTGGCCTCTGTCTTCTGGGAATAAAGCAGGGTTTCCTACTTCAGG
GGATGTAGAGAGATGCCCAGGTTGCACAGGAGTGGGATGGGGTGTGGTAGCAAAAGGAGGGAGAGGAGTC
CTTTTTGTGCCAAATCCCTAAGTGCCGTTCGGGGGCCATGTGTGCAGCATGACTCTCCCTGTCTGTGGCA
GGGACCCAAGCGCTTGCTTAAGCCCCAGTGCTCCATGCCAGCACTTGAACTGTCTGGGGTTTGATGGACA
GAGGCTGAGGAATTTCCTGGCTTCCCCAGATAGTGTCCTGGGACATGGTATGCTTTGGGGCTGGGGTAGC
ATGGAATCCCTCTGAGGACCTGGATACTGGTACTACGGGGTGGGGAAGAGGAACCTTAAACTTGGCTTTC
CCCAGCCTTCAGCCTGAGTCTAGCATGTTTCTAGCTCCCCAGTCCCTTGTGAAGCCTTGAGGGCTGGCAG
AAGGGTTAGGAGGTTGAACTCTAGATTCCCTTCCTGTCTTTGCCTTCCTTTTACCCCTTTCCCTGCAACC
TCCTTGACTCTGGCCTGAATTTGTTGGTGCCTCAGTTTCTCTGTCTGTACCTATTTAAGCCAAAGGCACT
AGCCTGAATTTTGCTTGAAGATCACTTTGTCTTGGAAATGACTAGAGAGGCAGAGGAGAAGGGTTTCCAG
AGTTGCTAGGTTTGGGAGTGGAAGGGGCAGGCAGTGCACTTGCCCCTCCTCATGCCCCTTCTGACACCAG
CTCCCTGTGGAGGCCTGGTTTCTGGGTAATGCCTCCCTTGGGCATCTTCATGCATCAACCAAATGGGCCA
TCAGGTACTTCATTAGTCATGGCAGAAGGAGGGGAAAAGACTTGTTTTCCAGACAGAAAATCTACTCCCC
TGTCCCCAGCCATATCCCTGGATAGGAAGGGATAGGAAGAGACTACTTGGTGCCATGGGGTAGGGGTGAG
GGTATAAGTAGATCAGAGTGGGAAGACCTCAGCCTTGGGTGGCTTGTCTCTGCTTCTTGCCAGGTGGGAG
GGCCTGTCCACACCCTGGATCCCCGTACCACAGTGCCAGCCATGCCCTTCCCCTGGGCTACCATTGTCCC
TTTCCTCACCCAGTTGGTAGAGGAGTCAGGAGGTGGGAGGCCGTGGGCTTTGGTTTTATAATGTAACCAC
TGTGGGGGTGGGGGAGGATGGTGAACCATGTATTTCAGTGAAATATTTAATATATTTAAATATCAATAAA
ATCAAACTCTTTGT

>gi|4557256|ref|NM_001115.1| Homo sapiens adenylate cyclase 8 (brain) (ADCY8), mRNA
GACTGGCTGCAGCCGCAGTCTTGGTGGAGGAGGTGGTGACCACCACCGCTCCTCCACCTGCATCCGGCTG
CGGGACTGCGGCGGCCGCGTTTGCCCTGCAGACCCTGCACCCCGGGACGCGGCTCATCTGTCATTAGCAC
CGGCACTAAGCTCCCACCGCTCAGCGACTTGGTCCGCCGCAAGCTCCGCCGCAGGCTTTGTCCGCTAGCG
CTCGGCTGAGTCTGGGCGGGCGGGAAACCTGGGCTAGGGCGAGGCGGGGCCCCTGGACATGCCTTTCTCC
ACGTCCGCCTCCTCGACCCTATTGTAAGCGGAGAAACTTAGTGTGCGAGGCAGGCAGGGGACGTCCCCAT
TTTGATGTCCCGTACCCTCCACCCCCTTCGGATCGAGGTAGTAAAGAGGCTCCTGTAGGAAACTGACTGC
CTCTATGATTGCGGCCTCTTGGGGGATTTTGCGTTTAGCCCGAAAGTTGGCTTTGCCAAAAGACGCACGG
GTAGGAAGGGCGAAAAGGAAACCCTGTATTCCGTCGCGCTGGGCTCTCCGAGTCCGTGCGCAAAGCGGCC
TACGAGTCCTGGCTCCGCACCTGCAGAGGACAAGAGCCAATGCCTAAAAAAGAACAGCGGAGGAACCGGC
TGGCGCGGCCAGCTGGAACGCTGGATCGCAGTGCGCCCAGGGAAGGCCGGGGGCGCCCGCCGGCCCTAGC
CCTCAGTGGTCCTCTCCCACGCCGGCCCGCGCGTGCCTCTGCCTACAAGACCTGGGGCGTCCTGGCCAGA
TCTGGATGGCAGGTCCCTCCGCCACCCCCGGCCCGGTTCCGGGGGCGTGGCTTGGCGCGGGGGCGGGTTT
AAGTCACCGCGGGTGTCTGACCACTCTGACAGGTCTCCAAATTTCTCCCAGTCGCCTGGCGCCCGCGGTG
CGTTTCAGAGCTCCAGGGTGGCACGCGGCGGCGCTTCCCTAGATCCAGAGGCGTCTCTGTCGACTTCCAC
GCGGCCTCGGGCCTCCCTTCTCCTCCAAACCTTCGCCTCATCCGCCAAGCTTCGGTTCTCAGCCTCAGAT
ATCCGCACCGGCGGCTTCTCTTCGTTCTCGGAGCTCTTGGCTTTGGAGCCCTCACCACTTTTTCCTTCCC
CCGCCTCTCCTGATCCTCCTAGCTCCGAGCCAAATGGACTCCAAAGAACGAAATAAAGGGGATGAGAACT
GTGTGCTGCGACCCTTCGAAAGCACAGCTGAAAGCGTTGACCTCGTCTTATAGATCAGGCTGGGACCCTG
GGGCGAGAGTCCCCACACCCCCTCCGGGAGGGATGCTTCTGGCCAGAGCCAGCGCTGCGCTGTCAGTCCT
TGCTCCCGAACTAGGAAAGAGCCTAGGAGGGAGCCTCAGCATACCCCTTCCTCCAAATTAACTATTTGGT
GAATTGTTAGCGCCGAGGCTACCACCTCTCCAACCCTGTCGCGGGGCGCGCCGCCACCTCACCGTGACCC
CCTCCTCCTCCTTCTTTGCCACCGCCCCCAGCTCCGCCCCTGCTCCCCATCCCGGCGCAATGGAGTTCTC
CGAAGGGCGATGATTCCAGCCACATCTGCTAACTTCGCACCCATCGCTGCCGCCGGTCACCGCCGGCCAG
GCCCCCTGCAGCCGCGGAGCAGTGGGCGTCCAAAGCCCAGTGCAGCAGCCAGGACCCGCCCGACGCGCAG
CAGAAGCACGGCGCCCAGGCGCTTAGGCGTCTCTTGGAGAGCAAAGGCTGCGCCAAAACGCTGAGCCTAG
AATCAACCAAGGAGCCTGAGCCCAGGAAGGGGCTGCGTGGCTCACAGCGCTGCGGCTCCTGAGGACAAAT
AGCCACTGCCGCTGCGTACCCAAGCTGCGCCGGCTGGCGGGAGAGCAGCACGCAAGGACGCCGAGGTCCG
CCGCGATCTTCCAGGTGCCCTTTGCCCCTGGGCACAGTATGACCCGACCTACAGGGAGCCCTAGCGCAGG
GCTCCTGCAACGGGTCAGCCTAGGATAAAAAGGATCCTTGCCAAGCTCCTACCAGGCCGCCTTTGAGTCT
TTAGGAACCCCTCCTCCGGCTGCCTCCCCAAGGTTCTGGGCCTCCTTCCCTGCGGCCCAGAGCCATGGAG
CTCTCCGATGTGCGCTGCCTTACAGGCAGCGAGGAACTCTACACCATCCACCCGACGCCCCCGGCCGGCG
ACGGCAGGAGCGCCTCCCGGCCGCAGCGGCTGCTGTGGCAGACGGCGGTGCGACACATCACGGAGCAGCG
CTTCATTCACGGGCACCGGGGAGGCAGCGGCAGCGGGAGTGGAGGCTCGGGCAAAGCCTCGGACCCTGCG
GGCGGCGGCCCCAACCACCACGCGCCGCAGCTGTCAGGCGACTCGGCGCTGCCCCTCTACTCGCTGGGCC

CGGGAGAGCGAGCGCACAGCACCTGCGGCACCAAAGTCTTCCCGGAACGCAGCGGGAGCGGCAGTGCCAG
CGGCAGCGGAGGCGGGGGCGACCTGGGCTTCCTGCACCTTGACTGTGCCCCTAGCAACTCGGATTTCTTT
CTTAATGGGGGCTATAGCTACCGAGGGGTCATTTTCCCCACCCTGCGCAACTCCTTCAAATCTCGGGATT
TGGAACGCCTCTACCAGCGCTATTTCTTGGGCCAAAGGCGCAAATCGGAAGTGGTGATGAACGTGCTGGA
CGTGCTGACCAAACTCACTCTCTTGGTCCTACACTTGAGCCTGGCCTCGGCCCCCATGGACCCGCTCAAG
GGCATCCTGCTGGGCTTCTTCACCGGCATTGAGGTAGTGATCTGCGCCCTGGTGGTGGTCAGGAAGGACA
CCACCTCCCACACGTACCTGCAGTACAGCGGCGTGGTCACCTGGGTGGCCATGACCACCCAGATCCTGGC
AGCAGGCCTCGGCTACGGGCTCCTGGGCGACGGCATAGGCTACGTGCTCTTCACGCTCTTCGCCACCTAC
AGTATGCTGCCGCTGCCGCTCACCTGGGCCATCCTGGCCGGCCTGGGCACCTCGCTGCTGCAGGTCATCC
TCCAAGTGGTCATACCCCGGCTGGCGGTCATTTCCATCAACCAGGTTGTGGCCCAGGCAGTGCTATTCAT
GTGTATGAACACAGCTGGAATCTTCATCAGTTACCTGTCAGACCGGGCCCAGCGCCAAGCTTTCCTGGAG
ACTCGGAGGTGTGTGGAGGCCAGGCTGCGCCTGGAGACAGAGAACCAAAGACAGGAGCGGCTCGTGCTTT
CTGTGCTCCCCCGGTTTGTTGTCCTGGAAATGATCAACGACATGACCAATGTGGAAGATGAGCACCTGCA
GCACCAGTTCCATCGGATCTACATCCATCGCTATGAGAACGTCAGTATTCTTTTTGCAGATGTTAAAGGA
TTTACCAACCTCTCCACGACCTTGTCTGCTCAGGAGCTGGTCAGGATGCTCAACGAGCTCTTTGCCAGAT
TTGATCGACTGGCCCATGAGCATCACTGCCTTCGTATTAAAATCCTGGGGGACTGCTACTACTGCGTGTC
TGGACTTCCTGAGCCCCGCCAGGACCATGCCCACTGCTGTGTTGAAATGGGTCTCAGCATGATCAAAACC
ATCAGGTATGTGCGGTCAAGGACAAAACACGATGTTGACATGAGGATTGGAATCCACTCCGGCTCGGTGC
TGTGCGGTGTTTTGGGACTACGGAAGTGGCAGTTTGATGTCTGGTCTTGGGATGTGGATATTGCAAACAA
ACTCGAATCTGGAGGAATCCCCGGGAGGATTCACATTTCCAAAGCCACGCTGGACTGTCTCAACGGTGAC
TATAACGTGGAAGAGGGCCATGGTAAAGAGAGGAATGAATTCCTGAGGAAGCATAATATCGAAACTTACT
TAATTAAGCAGCCTGAGGACAGTCTGCTGTCCTTGCCTGAAGATATCGTCAAGGAGTCAGTGAGCTCCTC
AGACCGGAGAAACAGTGGGGCCACATTCACTGAAGGATCCTGGAGCCCTGAACTGCCCTTTGATAATATC
GTGGGGAAACAGAATACTCTGGCTGCCCTAACAAGAAATTCAATAAATCTGCTTCCAAACCATCTTGCAC
AAGCTTTGCATGTCCAGTCTGGGCCTGAGGAAATTAACAAGAGAATAGAACATACCATCGACTTGCGGAG
TGGCGATAAATTGAGAAGAGAGCATATCAAGCCATTCTCACTGATGTTTAAAGACTCCAGCCTGGAGCAC
AAGTATTCTCAAATGAGGGATGAAGTGTTCAAGTCAAACTTGGTCTGTGCATTTATCGTTCTTCTATTTA
TCACGGCAATACAAAGTTTGCTTCCTTCTTCAAGAGTGATGCCAATGACCATCCAGTTCTCCATTCTGAT
TATGCTGCACTCGGCTCTGGTCCTCATCACCACAGCAGAGGATTATAAATGTTTGCCCCTCATCCTCCGG
AAAACTTGCTGTTGGATTAATGAGACCTATTTGGCCCGGAACGTCATCATCTTTGCATCCATTTTGATTA
ATTTCCTGGGTGCCATCTTAAATATCCTGTGGTGTGATTTTGACAAGTCGATACCCTTGAAGAACCTGAC
TTTCAATTCCTCAGCTGTGTTTACAGATATCTGCTCCTACCCAGAGTACTTTGTCTTCACGGGGGTGTTG
GCCATGGTGACCTGTGCAGTTTTCCTCCGGCTGAACTCCGTCCTGAAGCTGGCAGTGCTGCTGATCATGA
TTGCCATCTATGCCCTGCTCACTGAGACCGTCTACGCAGGCCTCTTTCTGCGTTATGACAACCTCAACCA
CAGTGGAGAAGATTTCCTGGGGACCAAGGAGGTATCACTGCTACTGATGGCCATGTTCCTCCTGGCTGTG
TTCTACCATGGACAGCAGCTGGAGTACACAGCCCGCCTGGACTTCCTTTGGCGAGTACAGGCCAAAGAGG
AGATCAATGAGATGAAGGAGCTGAGGGAACACAATGAGAACATGCTCCGGAATATCTTACCCAGCCATGT
GGCCCGCCATTTCCTAGAGAAGGACCGAGACAATGAGGAGCTGTATTCTCAATCCTATGATGCTGTTGGG
GTGATGTTTGCCTCCATCCCAGGATTTGCGGACTTTTACTCTCAGACTGAAATGAATAACCAGGGAGTGG
AATGCCTGCGCTTGCTCAATGAGATCATTGCTGACTTCGATGAGTTGCTTGGTGAAGACCGATTTCAAGA
CATTGAAAAGATTAAGACCATTGGCAGCACCTACATGGCCGTGTCAGGCCTGTCACCTGAAAAACAGCAA
TGTGAAGACAAGTGGGGACATTTGTGTGCTCTGGCTGACTTCTCACTCGCCCTGACAGAAAGCATACAGG
AGATCAACAAGCATTCATTCAACAATTTTGAACTCCGGATTGGCATCAGCCACGGCTCAGTGGTAGCTGG
CGTTATCGGCGCTAAGAAACCACAGTATGACATTTGGGGCAAAACTGTGAACCTGGCAAGCCGAATGGAC
AGCACGGGGGTTAGTGGCCGGATCCAAGTCCCAGAGGAGACCTATCTCATCCTGAAGGACCAGGGCTTTG
CCTTTGATTACCGAGGGGAGATCTATGTGAAGGGTATCAGTGAACAGGAAGGAAAAATCAAAACGTACTT
TCTTCTGGGAAGAGTCCAACCCAACCCATTCATCTTGCCCCCAAGAAGACTGCCTGGGCAGTACTCCCTG
GCCGCGGTTGTCCTGGGACTTGTCCAGTCCCTCAATAGGCAAAGGCAGAAGCAGCTACTCAATGAGAACA
ACAACACAGGAATCATCAAGGGTCATTACAACCGGCGGACTTTGTTGTCACCCAGCGGCACAGAGCCTGG
AGCCCAGGCTGAAGGCACCGACAAATCTGATTTGCCATAAAAGCATTTTCTTTCTGTTTTTTTTTTTTTT
TGTATTTCTTTTATATATAAAATAAATATACTAATAAAAAGGTTTAATTTTTTTTAGAACAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACCCCAAAAAAAAAAAAAAA

>gi|7661961|ref|NM_014770.1| Homo sapiens centaurin, gamma 1 (CENTG1), mRNA
AAGGGGCCTTCTGAGGTTTGGGGGCTGTAGGGCCATGGGCCTCAGGGCCAGAGGTGGTTGTTAGCCTGGC
AAGACAGGTCTGGGCAACATGCATGCCCAGAGGCAGTTCGTTGTAGCTGCAGTGAGAGCAGAAGTCAGAC

GACATGAGGTGGCCAAGCAGGCTCTAAACCGCCTCAGGAAGCTGGCAGAGAGGGTGGACGACCCCGAACT
CCAGGACAGCATCCAGGCCTCATTGGACAGCATTCGAGAGGCTGTGATCAATAGCCAGGAATGGACTTTG
AGCCGCTCCATTCCTGAACTGCGCCTGGGTGTGCTGGGCGATGCCAGGAGTGGGAAGTCATCGCTCATCC
ACCGATTCCTGACTGGCTCATACCAGGTGCTGGAGAAGACAGAGAGTGAGCAGTACAAGAAAGAAATGTT
GGTGGATGGACAGACACATCTGGTGCTAATCCGAGAGGAAGCTGGGGCACCTGATGCCAAGTTCTCAGGC
TGGGCAGATGCTGTGATCTTCGTCTTCAGCCTGGAGGATGAGAACAGTTTCCAGGCTGTGAGCCGTCTCC
ATGGGCAGCTGAGTTCCCTTCGCGGGGAGGGACGAGGAGGCCTGGCCTTGGCACTGGTGGGGACACAAGA
CAGGATCAGTGCTTCCTCCCCTCGGGTGGTGGGAGATGCTCGTGCCAGAGCTCTGTGCGCGGACATGAAA
CGCTGCAGCTACTATGAGACTTGTGCAACCTATGGGCTCAATGTGGATCGGGTCTTCCAGGAGGTGGCCC
AGAAGGTGGTGACCTTGCGCAAGCAGCAACAGCTTCTGGCTGCCTGCAAGTCCCTGCCCAGCTCCCCAAG
CCACTCAGCTGCATCCACTCCGGTAGCTGGCCAGGCTAGTAACGGGGGCCACACTAGCGACTACTCTTCT
TCCCTCCCGTCCTCACCGAATGTTGGTCACCGGGAGCTCCGAGCCGAGGCAGCTGCAGTGGCTGGATTGA
GCACCCCAGGGTCCCTGCACCGGGCAGCCAAGCGCAGGACCAGCCTTTTTGCGAATCGTCGGGGTAGTGA
CTCCGAGAAACGAAGCTTGGATAGTCGGGGAGAGACAACAGGGAGTGGGCGAGCCATCCCCATCAAACAG
AGCTTCCTACTAAAACGAAGTGGCAATTCCTTGAACAAAGAATGGAAGAAGAAATATGTAACCCTGTCCA
GTAATGGCTTTCTACTCTACCACCCCAGTATTAACGATTACATCCACAGTACCCACGGCAAGGAGATGGA
CTTGCTGCGAACAACAGTCAAAGTCCCGGGCAAGCGGCCCCCGAGGGCCATCTCTGCCTTTGGCCCCTCA
GCCAGCATTAACGGGCTCGTCAAGGACATGAGCACTGTCCAGATGGGTGAAGGCCTGGAAGCCACTACTC
CCATGCCAAGCCCTAGCCCCAGCCCCAGTTCCCTGCAGCCACCACCAGATCAGACATCCAAACACCTGCT
GAAGCCAGACCGGAATTTGGCCCGAGCCCTCAGCACGGACTGTACCCCATCTGGAGACCTGAGCCCCCTG
AGTCGGGAACCCCCTCCTTCTCCCATGGTGAAGAAGCAGAGGAGGAAAAAATTGACAACACCATCCAAGA
CTGAAGGCTCGGCTGGGCAGGCTGAAGAGGAAAACTTTGAGTTCCTGATCGTGTCCAGCACGGGTCAGAC
GTGGCACTTTGAGGCAGCCAGTTTTGAGGAGCGGGATGCCTGGGTCCAGGCCATCGAGAGTCAGATCCTA
GCCAGTCTGCAATGCTGTGAGAGCAGCAAGGTCAAGCTGCGCACAGACAGCCAAAGCGAGGCCGTGGCCA
TCCAGGCGATCCGGAACGCCAAGGGGAATTCAATCTGCGTGGACTGCGGGGCCCCCAACCCCACGTGGGC
CAGCTTGAACCTGGGCGCCCTCATCTGCATCGAGTGTTCTGGCATCCACCGCAACCTGGGCACACACCTG
TCCCGCGTTCGCTCGCTGGACTTGGACGACTGGCCACGGGAGCTGACCCTGGTGCTGACGGCTATTGGCA
ACGACACGGCCAACCGCGTGTGGGAAAGCGACACGCGAGGCCGTGCCAAGCCCTCGCGGGACTCTTCGCG
GGAGGAGCGCGAGTCGTGGATTCGCGCCAAGTACGAGCAGCTACTGTTCCTGGCGCCGCTGAGCACCTCG
GAGGAGCCGCTGGGCCGCCAGCTGTGGGCCGCCGTGCAGGCCCAGGACGTGGCTACCGTTCTCCTGCTTT
TGGCCCATGCGCGACACGGGCCGCTCGACACCAGCGTAGAGGACCCACAGCTGCGCTCCCCACTCCACCT
GGCGGCCGAGCTCGCCCACGTCGTCATCACGCAACTGCTGCTGTGGTACGGCGCGGACGTGGCGGCCCGT
GACGCCCAGGGCCGCACGGCGCTGTTCTACGCCCGCCAGGCTGGAAGCCAGCTGTGCGCCGACATCCTTC
TCCAGCACGGCTGCCCGGGTGAGGGCGGCAGCGCGGCCACCACGCCCAGCGCGGCCACCACGCCCAGCAT
CACCGCCACGCCCAGCCCCCGCCGCCGGAGCAGCGCCGCTAGCGTGGGCCGCGCCGACGCCCCGGTTGCG
CTGGTATAGTTGCCCAGCGGGAGAGACACCCCCATCCCCACGCGGGCCGGGCACGACCACACCGGGCGGA
CCGCTGGACAGACGCACCCACTCACCTCTCCGATCCGCACCCCGCCCCACGGGAGCACTTCCTACCCCCA
CGAGGGCACAGCCCCCACGCCTTCCAGAAGACACAAACTCACCTCCCTCTCCCCAACGAGGCATGGAGAC
CCCAGCTCAACACGCCCCCTCTCCATTGTTTCCACACTCGGATTGCTCTGGGTCTACCCGCTCGGGGTTC
GCGGAAGGGGAGGTCCCCAGCGGTACGGGCTCCTAGGCGCTTGGACATGCCCGCTTGTGCCCCCTAGGGG
CGGAAAGAAGACCCGGTCCTGCCCGAGCTCAACAATCCCAGGGCGGGAGCCCATACCCAGGCTGGCTCCT
GGGGCGACGCCACGCCAGAGGGAGGGTTTAGTACATGGGAGGGCTAGCCCCGGGACTTGGGGCCAATACG
GAAACCCTACCCCTTCCATGCTCATCTCACTGCCCAGTGAAGGGGGCAAGGGCAGCGAGGGGCAGGACCC
CTGCTGCTCATGGGGGTGGGGGTTCCCAACCCTTTCCGTGAAAGGGACCGTGAGTAGTGGAAACCAGGAC
GTCCCCTACACCTACCCATGGGTGGAAGCTAAAGAGTCCGGGGGGAACCAAGAGCCTGGGTCCCTCCCAC
TACTATCTTGGGAGGGAGAAGGGATGGAGCAGGAGCGGGCTAAGAGGGCTGCGGGGGCCTTGTAATTTAT
TGCTTTGTTCCCCAACATGGGGATGGGGGCGGGCAGGGGCGTGGGGAGGGCGTTTTGGGGTAGGGGAAGC
CCAGGGTGGGCAGGGGGTGGGTTGGGGTGGGGGTGCTCTCGGGTTGTGTCTGTGACCGTGACTGCGTACC
TGTGACTGTGCAGCGCCCGTGGTGATCTGGGGTAGGGGGCACCCCTACAGTGGGACCCCTCCCCCATTAT
TCTTTCTGTCCAGCCCCTCCCTCCCACTGGAGCAGCTCCAGAGCCATTCCTCACCCCCGTGACCTCTCCC
AGCCAGGGCTGAGAGGATTCGAGGTGGCTGGGAGGGTTTCCAGGCCCCCTGCCCCTTCCCCACAAACTGG
GTGATAGGGCGGACTTACCTGGCCCAGCCCTGCCTCCCTCAGCCAACCCAGCCCTTGGGCTGTCTGTGTC
AGTGGTTTCCGGTCTTTTTTTTTTTTTTTTTTTCTGGCTAAAATAGTTTGCAAAGGACCAGGTAATTGGG
GAGGGGAGAGAGGTGGGGGCAAGGGGGAAATGCCCCCCCATCTCCTTGGAGGCAGTGGTGTGAATCTTCT
TCAACAGCAATTAAAGAGGAAGTGATTTTG

>gi|7662483|ref|NM_014914.1| Homo sapiens centaurin, gamma 2 (CENTG2), mRNA

CAAGGCGCCTGCGACTCGGTCCCAGGTCGGCGGCGGCGCGCGGCGGGCTCGCGCGGGGGCCCCGGCGCG
CCGGGCGGCGCAGTACGCAGCGCGCGGACCCACGCCACGGCCAGGAGCCCAGAGCAGCGCGGCCACACTG
CCCAGGGGTCGGCCCTCGGCCCCGGCGCTCGGAGCGCGGCGGCTGCCTGGGCTTTAATGGCTGCTCCGCG
GAGCAGCGCCTAGGGCTGGAAGGCGGCTGCGGCTCAGGAAGTCACCCGAGCAAGCCTCCTTCGGGGCCGG
CCGCACCCGCCGCGGCGCGCTCCATGGGGGCGCGCTCCCCCCGGGCGGCCCGCTGACCCGGGACGCCGGG
GCCCGCTCGCTCGCCGGCCGCGCGTCCCGGCCATGAACTGAGCCCGCGGGCCAGCCCCGCGCCTGCTCCG
CCCGCGCCTTTCTTCTCGCGCCTCCTCCGCCCGCCGCCGGCGGGCCCGGCTCCCCGGGGGCTGCGGCGCC
CCGGGCTCGGCGGCCCGCGGGCCCCGGGGCGCGGGGCGGCGGCGGCGGGGGGCGCGCGGCTCCGGGCGCG
GCGCCTGCACCATGAACTACCAGCAGCAGCTGGCCAACTCGGCTGCCATCCGGGCCGAGATCCAGCGCTT
CGAGTCGGTCCACCCCAACATCTACTCCATCTACGAGCTGCTGGAGCGCGTGGAGGAGCCGGTGCTGCAG
AACCAGATCCGGGAGCACGTCATCGCCATCGAAGATGCCTTCGTGAACAGCCAGGAATGGACGCTGAGTC
GATCTGTCCCGGAGCTCAAAGTGGGAATTGTGGGTAACTTGGCCAGCGGCAAGTCTGCCCTGGTGCACCG
GTACCTGACGGGCACATATGTCCAGGAGGAGTCTCCGGAAGGTGGCAGGTTCAAGAAAGAGATTGTCGTT
GATGGACAGAGCTATCTGCTGCTGATCAGAGATGAAGGGGGCCCCCCGGAGGCGCAGTTTGCCATGTGGG
TGGACGCTGTTATATTTGTCTTCAGCTTGGAGGATGAAATAAGTTTCCAGACCGTTTACCACTACTACAG
TCGAATGGCCAACTATCGGAACACGAGCGAGATTCCTCTGGTTCTGGTGGGAACCCAGGATGCCATAAGT
TCTGCTAACCCGAGGGTCATCGATGACGCCAGGGCGAGGAAGCTCTCCAACGACCTGAAACGGTGCACGT
ACTACGAGACGTGTGCTACATACGGGCTGAATGTGGAGAGGGTCTTCCAGGACGTTGCCCAGAAGATTGT
TGCCACAAGGAAGAAGCAGCAGCTGTCCATAGGACCCTGCAAGTCGCTACCTAATTCTCCCAGCCATTCC
TCCGTCTGTTCCGCGCAGGTGTCTGCCGTGCACATCAGCCAGACAAGTAATGGAGGTGGGAGTTTAAGCG
ACTATTCCTCCTCCGTTCCATCGACTCCCAGCATCAGCCAGAAGGAACTTCGGATCGATGTTCCTCCCAC
TGCCAACACGCCCACGCCCGTTCGCAAGCAGTCTAAGCGCCGGTCCAACCTGTTCACCTCTCGGAAAGGG
AGCGACCCAGACAAAGAGAAGAAAGGCCTGGAGAGTCGTGCGGACAGCATTGGGAGCGGCCGAGCCATCC
CAATTAAACAGGGCATGCTGTTGAAGCGAAGTGGCAAATCGTTGAATAAAGAGTGGAAAAAGAAATATGT
CACCCTGTGTGACAATGGCGTGCTGACCTATCATCCCAGTTTACATGATTACATGCAGAATGTTCATGGT
AAGGAGATTGACCTTCTGAGAACCACTGTGAAAGTCCCAGGGAAGAGGCCACCCCGAGCCACGTCAGCCT
GCGCACCCATCTCCAGCCCTAAAACCAATGGCCTATCCAAGGACATGAGCAGTTTACACATCTCACCCAA
TTCAGACACAGGGCTGGGTGACTCCGTATGCTCCAGCCCCAGTATCTCCAGCACCACCAGCCCCAAGCTC
GACCCGCCCCCCTCCCCTCACGCCAACAGAAAGAAGCACCGAAGGAAGAAAAGCACTAGCAACTTCAAAG
CCGACGGCCTGTCCGGCACTGCTGAAGAACAAGAAGAAAATTTTGAGTTTATCATTGTGTCCCTCACTGG
CCAAACATGGCACTTTGAAGCCACGACGTATGAGGAGCGGGACGCCTGGGTCCAAGCCATCGAGAGCCAG
ATCCTGGCCAGCCTGCAGTCGTGCGAGAGCAGCAAGAACAAGTCCCGGCTGACGAGCCAGAGCGAGGCCA
TGGCCCTGCAGTCGATCCGGAACATGCGCGGGAACTCCCACTGTGTGGACTGCGAGACCCAGAATCCCAA
CTGGGCCAGTTTGAACTTGGGAGCCCTCATGTGCATCGAATGCTCAGGGATCCACCGGAATCTTGGCACC
CACCTTTCCCGAGTCCGATCTCTGGACCTGGATGACTGGCCAATCGAGCTCATCAAGGTGATGTCATCCA
TCGGGAACGAGCTAGCCAACAGCGTCTGGGAAGAGAGCAGCCAGGGGCGGACGAAACCATCGGTAGACTC
CACAAGGGAAGAGAAGGAACGGTGGATCCGTGCCAAGTACGAGCAGAAGCTCTTCCTGGCCCCGCTGCCC
TGCACGGAGCTGTCCCTGGGCCAGCACCTGCTGCGGGCCACCGCCGACGAGGACCTGCGGACGGCCATCC
TGCTGCTGGCACACGGCTCCCGGGACGAGGTGAACGAGACCTGCGGGGAGGGAGACGGCCGCACGGCGCT
GCATCTGGCCTGCCGCAAGGGGAATGTGGTCCTGGCGCAGCTCCTGATCTGGTACGGAGTGGACGTCACG
GCCCGAGATGCCCACGGGAACACAGCTCTGGCCTACGCCCGGCAGGCCTCCAGCCAGGAGTGCATCGACG
TGCTGCTGCAGTACGGCTGCCCCGACGAGCGCTTCGTGCTCATGGCCACCCCTAACCTGTCCAGGAGAAA
CAATAACCGGAACAACAGCAGTGGGAGGGTGCCCACCATCATCTGAGGAACAGCCGTGCCCGCCTGCTCG
CCGCACCTGGGACGCGGCAGCCTCGCCGCATTCTCGCTCAGAAGTCGCAGCACGTGAGTCCCGTCGCATC
CCCTCCCTCTTCCTGGTGGCCACCTCCCTCCCGCCCACCCACTCTCACCCCAAACAAAATCACAAAACCT
GGACATCCCTCAAGGGGCGAAGAGGCGGCCGGGAGACTGCAGAAGTGGCTCCTTTTCATAAACTCCCCTA
AACCACACACAGGAGAGAGCGACGGGCCTCGGCCCTTTGATGATAGCACATGGCGCAGGACCCTTGTCCT
GGTGGCACAAGGGATGGGGACGCGAGGGGGAGGGGAGGCGAGGAACAAGGAGAAGGGGCAACTTTCCTTA
ACTGGCAGTTGAGCACATAGTACATTTCCCCTCTACCAAACGGAACACTTGGATTCCATCTCTTCTCTGA
GGAGCTCGACGGCATAAATCAGAAGCAAGCACAGAGTTTGTCAGGTTTGAAGCCCCTATGATGGTGTGTG
TCAAATCAGTTGTAGCTAATCTGTCCAGGGAGAATACTGGCTTCATTACACTTGTACAGCCGAGTTCTTC
CCGCATTACTGCTGTTTAATAGAACGTGATTAGTCATCGCCGAGAAGAAAGCATATTAGCCGAGGAGGTA
GTCACGCGGCACGCGCCGGTGATTGCCACGATGTGATTGCAATACTCTTAGAAGCACCATATTATCCCAG
ACATGTTCTTTCAAGCCCTTGGAGCCCTCTCTAAATTCACTGTCATCATTTAGTATCTGTTTAATTTTTC
AGTCCAAAGAGAGGAAATCAGTCGCTGAGTATTATTTGACTCCGGTCTCCTTGGTGCAAAAACAAAATGG

GAAAAATAAATAAGAATAACTCAGAAACTCAAAAGGAAACCACAAATTCAGCTAATAATAGCATTTCGAG
TATATTTCGTAAACTAAGGAAATACACAAAAGGCTGTTTTTTTCCGACTGTAAGAGATATTTGATGTCCT
TTTGCCGAGGTGGATGTGTTAGTCTCAGGCCCTCCTGGACCACGTTGCCCAAGTCACACAGGCTTCTGTG
TTATGTATTTAGATAAGATGTGTGAAAATATATTTGAATAAAAGAAGTTCAT

>gi|32307157|ref|NM_031946.3| Homo sapiens centaurin, gamma 3 (CENTG3), mRNA
GCCATGAACTTCCAGGCGGGCGGGGGGCAGAGCCCGCAGCAGCAGCAGCAGCTGGCCGGCGGGCCCCCCC
AGCAGTTCGCGCTCTCCAACTCCGCGGCCATCCGGGCCGAGATCCAGCGCTTCGAGTCCGTGCATCCCAA
TATCTACGCCATCTACGACCTGATCGAGCGCATCGAGGATTTGGCGCTGCAGAACCAGATCCGGGAGCAC
GTCATCTCCATCGAGGACTCGTTTGTGAACAGCCAGGAGTGGACGCTGAGCCGCTCCGTACCGGAGCTTA
AAGTGGGCATAGTGGGGAACCTGTCTAGCGGGAAGTCAGCCCTGGTGCACCGCTATCTGACGGGGACCTA
TGTCCAGGAGGAGTCCCCTGAAGGGGGGCGGTTTAAGAAGGAGATTGTGGTGGATGGCCAGAGTTACCTG
CTGCTGATCCGAGATGAAGGAGGCCCCCCTGAGCTCCAGTTTGCTGCCTGGGTGGATGCAGTGGTGTTTG
TGTTCAGCCTGGAGGATGAAATCAGTTTCCAGACGGTGTACAACTACTTCCTGCGTCTCTGCAGCTTCCG
CAACGCCAGCGAGGTGCCCATGGTGCTTGTGGGCACGCAGGATGCCATCAGCGCTGCGAATCCCCGGGTT
ATCGACGACAGCAGAGCCCGCAAGCTCTCCACAGATCTGAAGCGGTGCACCTACTATGAGACGTGCGCGA
CCTACGGGCTCAATGTGGAGCGTGTCTTCCAGGACGTGGCCCAGAAGGTAGTGGCCTTGCGAAAGAAGCA
GCAACTGGCCATCGGGCCCTGCAAGTCACTGCCCAACTCGCCCAGCCACTCGGCCGTGTCCGCCGCCTCC
ATCCCGGCCGTGCACATCAACCAGGCCACGAATGGCGGCGGCAGCGCCTTCAGCGACTACTCGTCCTCAG
TCCCCTCCACCCCCAGCATCAGCCAGCGGGAGCTGCGCATCGAGACCATCGCTGCCTCCTCCACCCCCAC
ACCCATCCGAAAGCAGTCCAAGCGGCGCTCCAACATCTTCACGTCTCGGAAGGGTGCTGACCTGGACCGG
GAGAAGAAGGCTGCCGAGTGCAAGGTGGACAGCATCGGGAGCGGCCGCGCCATCCCCATCAAGCAGGGGA
TCCTGCTAAAGCGGAGCGGCAAGTCCCTGAACAAGGAGTGGAAGAAGAAGTATGTGACGCTCTGTGACAA
CGGGCTGCTCACCTATCACCCCAGCCTGCATGATTACATGCAGAACATCCACGGCAAGGAGATTGACCTG
CTGCGGACAACGGTGAAAGTGCCAGGGAAGCGCCTGCCCCGAGCCACACCTGCCACAGCCCCGGGCACCA
GCCCCCGTGCCAACGGGCTGTCCGTGGAGCGGAGTAACACACAGCTGGGTGGGGCACAGGTGCCCCCCA
CTCGGCCAGCAGCGCATCCCTGCACTCTGAGCGCCCCCTCAGCAGCTCGGCCTGGGCTGGCCCGCGCCCT
GAGGGGCTGCACCAGCGCTCCTGCTCCGTTTCCAGCGCCGACCAGTGGAGTGAGGCCACCACTTCCCTGC
CCCCAGGCATGCAGCACCCTGCCAGTGGCCCAGCTGAGGTACTCAGTTCCAGCCCCAAGCTGGATCCTCC
CCCATCTCCCCACTCCAACCGGAAGAAGCACCGGAGGAAAAAGAGCACCGGGACCCCCCGACCAGACGGC
CCCAGCAGTGCTACTGAAGAGGCAGAGGAGTCGTTTGAATTTGTGGTGGTGTCCCTCACTGGGCAGACGT
GGCACTTCGAGGCTTCAACGGCGGAGGAGCGGGAGCTGTGGGTTCAGAGTGTGCAGGCCCAGATCCTTGC
CAGCCTGCAAGGCTGCCGCAGTGCCAAGGACAAGACTCGACTGGGGAACCAGAACGCAGCTCTGGCTGTG
CAGGCCGTCCGCACCGTCCGCGGCAACAGCTTTTGTATCGACTGCGATGCACCCAATCCAGACTGGGCCA
GCCTGAACCTGGGTGCCCTGATGTGCATTGAGTGCTCAGGCATCCACCGACACCTGGGGGCTCACCTGTC
CCGGGTGCGCTCCCTTGACCTCGATGACTGGCCGCCTGAGCTGCTGGCTGTCATGACTGCCATGGGCAAT
GCCCTCGCCAACAGCGTCTGGGAGGGGGCCTTGGGTGGCTACTCCAAGCCAGGGCCTGATGCCTGCAGAG
AGGAGAAGGAACGCTGGATACGGGCCAAGTATGAACAGAAGCTCTTCCTGGCCCCACTGCCAAGCTCAGA
TGTGCCACTGGGGCAGCAGCTGCTCCGGGCCGTGGTGGAAGATGACCTGCGGCTGTTGGTGATGCTCCTG
GCACATGGCTCCAAAGAGGAGGTGAATGAGACCTATGGGGACGGGGACGGGCGGACGGCTCTACATCTCT
CCAGTGCCATGGCCAACGTTGTCTTCACGCAGCTGCTCATCTGGTACGGGGTGGACGTGAGGAGCCGGGA
CGCCCGGGGCCTGACTCCACTGGCATATGCTCGCCGGGCCGGCAGCCAGGAGTGTGCAGACATCTTGATC
CAGCATGGCTGCCCTGGGGAGGGCTGTGGCTTAGCGCCTACCCCCAACAGAGAGCCTGCCAATGGCACCA
ACCCCTCTGCTGAGCTGCACCGTAGTCCTAGCCTCCTATAAGGCCCAGGAAGAGGGCAGAGGGGCCAGAA
GGACTCCATGGCCCAAAGACCCTCCTCCCTGCAGGCACTGTGGGAACAGACACAGAGATGGAGAAGCAGG
GACATGCTGAGAGGACGAAGCCAAGGAAATTAGGGAGGAGAGTCAAAGGGATCAAGGAGAGTTGGGGATT
TGAGCTGCAGCAGAGAGGGATGAGGGATTTAGCCCTCTGCCCTAAGGTGCCATTGAAAAGGGACAGGACC
CTTCGGAGGTGCCTGTGAGGAGAGGGGAGCAGGACCTCTCCCTCCTCCAGATCCCTGCCTCCTAGTGCCA
GCCCCTCACACGCCTTCATCCTGAAACAGGAAGAGGACGGCACCAAGTTGGGGGTGCTGGATGAAAGAGA
CGAGGGGTGATCTGTGAGTCCCATGTAAACTTTGTACATTGGAATATTTATGTTTGTGTACATATTTGAT
GTGTGTGTGTATGATGAGCCAATAAACCAGACTGTGTGCGTGGCAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

>gi|13787202|ref|NM_006386.2| Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 (DDX17), transcript variant 1, mRNA
ATTTGTGCAGTCGCTGGGAAGGAAGGAGACGCCTAAACCGCGGCACTGCCCGGTTTGAGCGTAGCCAAA

CCTGCCCACCGGCTTTGTAGCCCCGATTCTCTGTGTTTGCTCCCGTCTCCGACGAGAGAGGCGGCGACG
GTGGCGTCTGCGACGGGAGACAGCGCGTCGGAGCGAGAGAGCGCTGCGCCTGCCGCCGCCCCAACAGCGG
AGGCGCCGCCGCCATCGGTCGTCACCAGACCGGAGCCGCAGGCCCTCCCGAGCCCGGCCATCCGTGCCCC
GCTCCCAGATCTCTATCCTTTTGGGACCATGCGCGGAGGAGGCTTTGGGGACCGGGACCGGGATCGTGAC
CGTGGAGGATTTGGAGCAAGAGGTGGTGGTGGCCTTCCCCCGAAGAAATTTGGTAATCCTGGGGAGCGTT
TGCGTAAAAAAAAGTGGGATTTGAGTGAGCTCCCCAAGTTTGAGAAAAATTTTTATGTGGAACATCCGGA
AGTAGCAAGGCTGACACCATATGAGGTTGATGAGCTACGCCGAAAGAAGGAGATTACAGTGAGGGGGGGA
GATGTTTGTCCTAAACCCGTGTTTGCCTTCCATCATGCTAACTTCCCACAATATGTAATGGATGTGTTGA
TGGATCAGCACTTTACAGAACCAACTCCAATTCAGTGCCAGGGATTTCCGTTGGCTCTTAGTGGCCGGGA
TATGGTGGGCATTGCTCAGACTGGCTCTGGGAAGACGTTGGCGTATCTCCTGCCTGCAATTGTTCATATT
AACCACCAGCCATACTTGGAAAGGGGAGATGGCCCAATCTGTCTAGTTCTGGCTCCTACCAGAGAGCTTG
CCCAGCAAGTACAGCAGGTGGCCGATGACTATGGCAAATGTTCTAGATTGAAGAGTACTTGTATTTATGG
AGGTGCTCCTAAAGGTCCCCAGATTCGAGACTTGGAAAGAGGTGTTGAGATCTGCATAGCCACTCCTGGA
CGTCTGATAGATTTCCTGGAGTCAGGAAAGACAAATCTTCGCCGATGTACTTACCTTGTATTGGACGAAG
CTGACAGAATGCTTGATATGGGGTTTGAACCCCAGATCCGTAAAATTGTTGACCAAATCAGGCCTGATAG
GCAGACACTGATGTGGAGTGCAACCTGGCCAAAAGAAGTAAGACAGCTTGCAGAGGATTTCCTTCGTGAT
TACACCCAGATCAACGTAGGCAATCTGGAGTTGAGTGCCAACCACAACATCCTCCAGATAGTGGATGTCT
GCATGGAAAGTGAAAAAGACCACAAGTTGATCCAACTAATGGAAGAAATAATGGCTGAAAAGGAAAACAA
AACAATAATATTTGTGGAGACAAAGAGACGCTGTGATGATCTGACTCGAAGGATGCGCAGAGATGGTTGG
CCAGCTATGTGTATCCATGGAGACAAGAGTCAACCAGAAAGAGATTGGGTACTTAATGAGTTCCGTTCTG
GAAAGGCACCCATCCTTATTGCTACAGATGTAGCCTCCCGTGGGCTAGATGTGGAAGATGTCAAGTTTGT
GATCAACTATGACTATCCAAACAGCTCAGAGGATTATGTGCACCGTATTGGCCGAACAGCCCGTAGCACC
AACAAGGGTACCGCCTATACCTTCTTCACCCCAGGGAACCTAAAACAGGCCAGAGAGCTTATCAAAGTGC
TGGAAGAGGCCAATCAGGCTATCAATCCAAAACTGATGCAGCTTGTGGACCACAGAGGAGGCGGCGGAGG
CGGGGGTGGTCGTTCTCGTTACCGGACCACTTCTTCAGCCAACAATCCCAATCTGATGTATCAGGATGAG
TGTGACCGAAGGCTTCGAGGAGTCAAGGATGGTGGCCGGAGAGACTCTGCAAGCTATCGGGATCGTAGTG
AAACCGATAGAGCTGGTTATGCTAATGGCAGTGGCTATGGAAGTCCAAATTCTGCCTTTGGAGCACAAGC
AGGCCAATACACCTATGGTCAAGGCACCTATGGGGCAGCTGCTTATGGCACCAGTAGCTATACAGCTCAA
GAATATGGTGCTGGCACTTATGGAGCTAGTAGCACCACCTCAACTGGGAGAAGTTCACAGAGCTCTAGCC
AGCAGTTTAGTGGGATAGGCCGGTCTGGGCAGCAGCCACAGCCACTGATGTCACAACAGTTTGCACAGCC
TCCGGGAGCTACCAATATGATAGGTTACATGGGGCAGACTGCCTACCAATACCCTCCTCCTCCTCCCCCT
CCTCCTCCTTCACGTAAATGAAACCACTCAAGTGGTAGTGACTCCAGCAGACTTAATTACATTTTAAGGA
ACACTGTCTTTCCTTTTTTTTTCCTCTTCGCCTTTTCTTTTTTTTTTCCTTTTTTCTTTTTTTTTTTTTT
AATTTTTCCCCCCAACCATCGTGATTTGTCTTTTCATGCAGATTAGTTAGAATTCACTGCCAGGTTTCTT
CTGCCCACCAAAATGATCCAGTCTGGAATAACATTTTGTAAAAAAAAAAAAAAAAAA

>gi|13514826|ref|NM_004396.2| Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (DDX5), mRNA
ACCTCATTCATTTCTACCGGTCTCTAGTAGTGCAGCTTCGGCTGGTGTCATCGGTGTCCTTCCTCCGCTG
CCGCCCCCGCAAGGCTTCGCCGTCATCGAGGCCATTTCCAGCGACTTGTCGCACGCTTTTCTATATACTT
CGTTCCCCGCCAACCGCAACCATTGACGCCATGTCGGGTTATTCGAGTGACCGAGACCGCGGCCGGGACC
GAGGGTTTGGTGCACCTCGATTTGGAGGAAGTAGGGCAGGGCCCTTATCTGGAAAGAAGTTTGGAAACCC
TGGGGAGAAATTAGTTAAAAAGAAGTGGAATCTTGATGAGCTGCCTAAATTTGAGAAGAATTTTTATCAA
GAGCACCCTGATTTGGCTAGGCGCACAGCACAAGAGGTGGAAACATACAGAAGAAGCAAGGAAATTACAG
TTAGAGGTCACAACTGCCCGAAGCCAGTTCTAAATTTTTATGAAGCCAATTTCCCTGCAAATGTCATGGA
TGTTATTGCAAGACAGAATTTCACTGAACCCACTGCTATTCAAGCTCAGGGATGGCCAGTTGCTCTAAGT
GGATTGGATATGGTTGGAGTGGCACAGACTGGATCTGGGAAAACATTGTCTTATTTGCTTCCTGCCATTG
TCCACATCAATCATCAGCCATTCCTAGAGAGAGGCGATGGGCCTATTTGTTTGGTGCTGGCACCAACTCG
GGAACTGGCCCAACAGGTGCAGCAAGTAGCTGCTGAATATTGTAGAGCATGTCGCTTGAAGTCTACTTGT
ATCTACGGTGGTGCTCCTAAGGGACCACAAATACGTGATTTGGAGAGAGGTGTGGAAATCTGTATTGCAA
CACCTGGAAGACTGATTGACTTTTTAGAGTGTGGAAAAACCAATCTGAGAAGAACAACCTACCTTGTCCT
TGATGAAGCAGATAGAATGCTTGATATGGGCTTTGAACCCCAAATAAGGAAGATTGTGGATCAAATAAGA
CCTGATAGGCAAACTCTAATGTGGAGTGCGACTTGGCCAAAAGAAGTAAGACAGCTTGCTGAAGATTTCC
TGAAAGACTATATTCATATAAACATTGGTGCACTTGAACTGAGTGCAAACCACAACATTCTTCAGATTGT
GGATGTGTGTCATGACGTAGAAAAGGATGAAAAACTTATTCGTCTAATGGAAGAGATCATGAGTGAGAAG
GAGAATAAAACCATTGTTTTTGTGGAAACCAAAAGAAGATGTGATGAGCTTACCAGAAAAATGAGGAGAG
ATGGGTGGCCTGCCATGGGTATCCATGGTGACAAGAGTCAACAAGAGCGTGACTGGGTTCTAAATGAATT

CAAACATGGAAAAGCTCCTATTCTGATTGCTACAGATGTGGCCTCCAGAGGGCTAGATGTGGAAGATGTG
AAATTTGTCATCAATTATGACTACCCTAACTCCTCAGAGGATTATATTCATCGAATTGGAAGAACTGCTC
GCAGTACCAAAACAGGCACAGCATACACTTTCTTTACACCTAATAACATAAAGCAAGTGAGCGACCTTAT
CTCTGTGCTTCGTGAAGCTAATCAAGCAATTAATCCCAAGTTGCTTCAGTTGGTCGAAGACAGAGGTTCA
GGTCGTTCCAGGGGTAGAGGAGGCATGAAGGATGACCGTCGGGACAGATACTCTGCGGCAAAAGGGGTG
GATTTAATACCTTTAGAGACAGGGAAAATTATGACAGAGGTTACTCTAGCCTGCTTAAAAGAGATTTTGG
GGCAAAAACTCAGAATGGTGTTTACAGTGCTGCAAATTACACCAATGGGAGCTTTGGAAGTAATTTTGTG
TCTGCTGGTATACAGACCAGTTTTAGGACTGGTAATCCAACAGGGACTTACCAGAATGGTTATGATAGCA
CTCAGCAATACGGAAGTAATGTTCCAAATATGCACAATGGTATGAACCAACAGGCATATGCATATCCTGC
TACTGCAGCTGCACCTATGATTGGTTATCCAATGCCAACAGGATATTCCCAATAAGACTTTAGAAGTATA
TGTAAATGTCTGTTTTTCATAATTGCTCTTTATATTGTGTGTTATCTGACAAGATAGTTATTTAAGAAAC
ATGGGAATTGCAGAAATGACTGCAGTGCAGCAGTAATTATGGTGCACTTTTTCGCTATTTAAGTTGGATA
TTTCTCTACATTCCTGAAACAATTTTTAGGTTTTTTTGTACTAGAAAATGCAGGCAGTGTTTTCACAAA
AGTAAATGTACAGTGATTTGAAATACAATAATGAAGGCAATGCATGGCCTTCCAATAAAAAATATTTGAA
GACTGAAAAAAAAAA

>gi|8922580|ref|NM_018173.1| Homo sapiens hypothetical protein FLJ10665 (FLJ10665), mRNA

AAGCGCCTCGCGGGGGTCTGGCCCGGAGTGGAGGGCGCGCGGTCCCAGCCCTCCCGCTCGGCCGGCGGGT
GTCGAGTTCAGCCCTAGGGGACCTCTTTCTCCTGGACATTGAAGATATGGCCCTTTGGAGGTGACCCAGG
AGAGAAGGGATGAAGGCCTTTGGTCCTCCACATGAGGGCCCCCTCCAAGGACTCGTGGCCTCCCGCATTG
AGACTTATGGGGGCCGGCATCGAGCCTCTGCTCAGAGCACTACTGGCAGACTCTATCCCCGAGGATACCC
TGTGCTGGATCCCAGTCGCCGACGCCTCCAGCAGTATGTCCCCTTTGCCAGGGGTTCTGGCCAGGCCCGA
GGCCTGTCACCCATGAGACTGCGAGATCCAGAGCCCGAGAAGAGGCACGGGGGCCATGTGGGGGCTGGCC
TGCTTCACTCCCCCAAACTCAAGGAACTCACCAAGGCCCATGAGCTGGAGGTGAGGCTGCACACTTTCAG
CATGTTTGGGATGCCCCGGCTGCCCCCTGAGGACCGGCGGCACTGGGAGATAGGAGAGGGTGGCGACAGT
GGCCTGACCATCGAGAAGTCCTGGAGGGAGCTGGTGCCTGGGCACAAGGAGATGAGCCAGGAGCTCTGCC
ACCAACAGGAGGCCCTGTGGGAGCTCCTGACCACCGAGCTGATCTACGTGAGAAAGCTCAAGATCATGAC
TGATCTGCTAGCCGCCGGCCTGCTGAACCTGCAGCGAGTGGGACTGCTGATGGAAGTGTCAGCTGAGACC
CTGTTTGGAAATGTCCCCAGCCTGATTCGAACCCACCGGAGCTTTTGGGATGAGGTGCTGGGGCCCACCC
TGGAGGAGACTCGGGCCTCGGGCCAGCCTCTGGACCCCATTGGTCTGCAAAGTGGCTTCCTGACGTTTGG
CCAGCGGTTCCACCCCTATGTCCAGTACTGCCTCCGAGTGAAGCAGACCATGGCTTACGCCCGAGAACAG
CAAGAAACTAACCCTCTCTTCCATGCCTTCGTGCAGTGGTGTGAGAAGCACAAGCGCTCTGGGAGGCAGA
TGCTCTGTGACTTGCTTATCAAGCCCCACCAGCGCATCACCAAGTACCCACTGCTGCTCCATGCTGTGCT
CAAGAGGAGCCCCGAGGCACGAGCCCAAGAGGCCCTGAATGCCATGATTGAAGCCGTGGAGTCATTCCTG
CGACATATCAATGGGCAGGTCCGCCAGGGCGAAGAGCAAGAGAGCTTGGCGGCTGCAGCACAACGCATCG
GGCCCTACGAGGTGCTGGAGCCACCCAGTGATGAGGTGGAGAAGAACCTGCGCCCATTCTCCACCCTGGA
CCTGACGTCCCCCATGCTGGGGGTTGCATCTGAGCACACCAGACAGCTGCTGCTGGAGGGGCCTGTGCGA
GTGAAGGAGGGACGAGAAGGGAAGCTGGACGTGTACCTGTTCCTCTTCTCTGATGTGCTCCTTGTGACCA
AGCCCCAGCGCAAGGCGGACAAAGCCAAGGTCATCCGACCCCCTCTCATGCTGGATAAGCTCGTGTGCCA
ACCCCTGCGAGACCCCAACAGCTTCCTGCTGATCCACCTCACTGAATTCCAGTGTGTCTCCAGCGCCCTC
CTTGTGCACTGTCCCAGTCCTACAGACCGTGCCCAGTGGCTGGAGAAGACCCAGCAGGCCCAGGCCGCCC
TACAGAAGCTGAAGGCAGAGGAGTATGTTCAACAGAAGAGGGAGCTCCTGACCCTCTATCGGGACCAGGA
CAGGGAGTCCCCCAGCACCAGGCCCTCCACGCCTTCCCTGGAGGGCTCTCAGAGCAGCGCAGAGGGGAGG
ACTCCTGAGTTCTCGACCATTATCCCCCACCTGGTGGTGACAGAAGACACAGATGAAGATGCTCCCCTTG
TGCCAGATGATACCTCAGACTCTGGCTACGGCACTTTGATCCCAGGCACCCCCACGGGGTCCCGCTCCCC
ACTGAGCCGTCTACGCCAAAGAGCCCTTCGGCGGACCCTCGCCTCACCTTCTCCACCCTGGAACTCCGG
GACATCCCTCTGCGTCCCCACCCTCCCGACCCCCAAGCTCCCCAACGCCGAAGCGCCCCCGAACTGCCGG
AAGGAATCCTAAAAGGAGGCAGTCTTCCCCAGGAAGACCCACCAACCTGGTCTGAGGAAGAAGATGGGGC
CTCCGAGCGAGGGAATGTGGTGGTGGAAACACTCCACAGGGCCCGGCTTCGGGGCCAGCTTCCCTCCTCC
CCAACCCATGCTGACTCTGCCGGGGAAAGCCCCTGGGAGTCCTCAGGGGAGGAGGAAGAAGAGGGGCCTC
TGTTCCTGAAAGCTGGCCACACATCCCTGCGCCCAATGCGGGCTGAGGACATGCTCAGAGAGATCCGGGA
GGAGCTGGCCAGCCAAAGGATTGAGGGGGCCGAGGAGCCCCGGGACAGCAGGCCACGGAAGCTGACTCGG
GCCCAGCTGCAGAGGATGCGGGGGCCCCACATCATTCAGCTGGACACCCCTCTGTCCGCATCAGAGGTAT
GAGGAATGCAGAGGACCTTTGGCATGCATCTCTCCCAGAGGAGATCTCTCCCCAGTAGTGCTGGTCACCC
TCCGGCATCTGTGACTCTACCTCAAGGACCACATTTCCCAAAGGAAGCCTGGCCCAGGCACCCTGCCTCC
TGCTCTGTTTGGGGATCAAGAACTGTAAATTTATGTATCATAGGTGCACCTGAGCCCCACAGAAAGTTGT

GCATAAAAATGACTGCCCTGGCTGGGCATGGCTGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGA
GGATCCCTTGAGCCCAGGAGTTCCAGACCAGCCTGGGCAATATAGGGAAACCCTGTCTTTACAAAAAAA
ATTTTAAAAATT

>gi|29728515|ref|XM_030970.9| Homo sapiens KIAA0720 protein (KIAA0720), mRNA
AAACTAAGGCCTTCCTGGTAGCCAAGGAGCCCAGCAGAGGGGCTGCTGCTGGCTGCTGGGATTGCAGAGG
CCGGGGTCTCTGTGGTGTTGCTTTCCTGGAAAGGAGGGACGGCACCTCCAGGGCAGCCAGCAGTGTGGGA
GCCCATTCCAGGGCGCAAATGGGCACTCAGGAATGGAAAATCCAAGAAGGAACCAACCACCAACAAGGAA
ATGCAGTGTGAGCGGCGGCTGCGAAGTCTGTGCCTTCAAATATACAGCGCCCAGGGGACCTGTGTTGGAC
GGGGAGCAAATTGGCAGGGCTGAGAGCGCCTTGGTTTTCTGTGCAGACAGGTCCAGCTGCAGAAATTAAG
ACTGGGGCTGAGTCGGGGAGAAGCCTTCCATGTTGAGATGGCAACTGGGCAAAGCAGGACGGAGACCTGT
GTGTCTGATTAGAGAGGCCTGTGGCATTGGCATGTGGCTGGAGGTCCAGGCAGGGTGCCACCACCGCAGA
GGTCAAGCATGAATTCAGTCCTGACAAAACATGGGTCTCCACCTCGAAGCTGGCTCAGCCTTTGTTCAGG
AACCGACGACCAGAGCCCCGCTGAAAAGAAGGGACTGCGCTGTCAGAACCCCGCCTGCATGGACAAGGGG
CGGGCGGCCAAGGTATGTCACCACGCCGACTGCCAGCAGCTGCACCGCCGGGGGCCCCTCAACCTCTGCG
AGGCCTGTGACAGCAAGTTCCACAGCACCATGCATTATGATGGGCATGTCCGCTTCGACCTTCCCCCACA
AGGCTCTGTGCTGGCCCGGAACGTGTCCACCCGGTCATGCCCGCCGCGCACCAGCCCCGCAGTGGACTTG
GAGGAGGAGGAGGAGGAGAGCTCTGTGGATGGCAAAGGGGACCGGAAGAGCACAGGCCTGAAACTCTCCA
AGAAGAAAGCAAGGAGGAGACACACGGATGACCCAAGCAAGGAATGCTTCACTCTGAAATTTGACCTGAA
TGTGGACATTGAGACAGAGATCGTCCCAGCCATGAAGAAGAAGTCACTGGGGGAGGTGCTGCTGCCTGTA
TTTGAAAGGAAGGGCATTGCGCTGGGCAAAGTGGACATCTACCTGGACCAGTCCAACACACCCCTGTCCC
TCACCTTCGAGGCCTACAGGTTCGGGGGACACTACCTTCGTGTCAAAGCCCCAGCCAAGCCTGGAGATGA
GGGCAAGGTGGAGCAGGGCATGAAGGACTCCAAGTCCCTGAGTTTGCCGATTCTGCGGCCAGCTGGGACC
GGGCCCCCCGCCCTGGAGCGTGTGGACGCCCAGAGCCGCCGGGAGAGCCTGGACATCTTGGCCCCTGGCC
GCCGCCGCAAGAACATGTCGGAGTTCCTGGGGGAGGCGAGCATCCCCGGGCAGGAGCCCCCCACGCCCTC
CAGCTGCTCTCTGCCCAGCGGCAGCAGTGGCAGCACCAACACTGGCGACAGCTGGAAGAACCGGGCGGCC
AGTCGCTTCAGCGGCTTTTTCAGCTCCGGCCCCAGCACCAGCGCCTTTGGCCGGGAGGTAGACAAGATGG
AGCAGCTGGAGGGCAAGCTGCACACCTACAGCCTCTTCGGGCTGCCCAGGCTGCCCCGGGGGCTGCGCTT
CGACCATGACTCCTGGGAGGAGGAGTACGATGAAGACGAGGATGAGGACAATGCCTGCCTGAGGCTGGAG
GACAGCTGGCGGGAGCTCATTGATGGGCATGAGAAGCTGACCCGGCGGCAGTGCCACCAGCAGGAGGCGG
TGTGGGAGCTGCTGCACACGGAGGCCTCCTACATCAGGAAACTGCGGGTGATCATCAACCTGTTCCTGTG
CTGCCTCCTGAACCTGCAAGAGTCAGGGCTGCTGTGTGAGGTGGAGGCGGAGCGCCTGTTCAGCAACATC
CCGGAGATCGCGCAGCTGCACCGCAGGCTGTGGGCTAGCGTGATGGCGCCGGTGCTGGAGAAGGCGCGGC
GCACGCGAGCGCTGCTACAGCCCGGGGACTTCCTCAAAGGCTTCAAGATGTTCGGCTCGCTCTTCAAGCC
CTACATCCGCTACTGCATGGAGGAGGAGGGCTGCATGGAGTACATGCGCGGCCTGCTGCGCGACAACGAC
CTCTTCCGGGCCTACATCACGTGGGCGGAGAAGCACCCACAGTGCCAGAGGCTGAAGCTGAGCGACATGC
TGGCCAAACCCCACCAGCGGCTCACCAAGTACCCGCTGCTGCTCAAGTCGGTGCTGAGGAAGACCGAGGA
GCCGCGCGCCAAGGAGGCCGTCGTCGCCATGATCGGCTCCGTGGAGCGCTTCATCCACCACGTGAACGCG
TGCATGCGGCAGCGGCAGGAGCGGCAGCGGCTGGCGGCCGTGGTGAGCCGCATCGACGCCTACGAGGTGG
TGGAAAGCAGCAGCGACGAAGTGGACAAGCTCCTGAAGGAATTTCTGCACCTGGACTTGACAGCGCCCAT
CCCTGGCGCCTCCCCGGAGGAGACGCGGCAGCTGCTGCTGGAGGGGAGCCTGAGGATGAAGGAGGGGAAG
GACAGCAAGATGGATGTGTACTGCTTCCTCTTCACGGATCTGCTGTTGGTGACCAAAGCAGTGAAGAAGG
CAGAGAGGACCAGGGTCATCAGGCCACCCCTGCTCGTGGACAAGATTGTGTGCCGGGAGCTACGGGACCC
TGGGTCCTTCCTCCTTATCTACCTGAATGAGTTTCACAGTGCTGTAGGGGCCTACACGTTCCAGGCCAGT
GGCCAGGCCTTGTGCCGTGGCTGGGTGGACACCATTTACAATGCCCAGAACCAGCTGCAACAGCTGCGTG
CACAGGAGCCCCCAGGCAGTCAGCAGCCCCTGCAGAGCCTGGAAGAGGAGGAGGATGAGCAGGAGGAGGA
AGAGGAGGAGGAGGAGGAGGAGGAGGAAGGCGAGGACAGTGGCACTTCAGCTGCCAGCTCCCCTACCATC
ATGCGGAAAAGCAGCGGCAGCCCCGACTCTCAGCACTGTGCCTCAGATGGCTCCACGGAGACCCTGGCCA
TGGTTGTGGTAGAGCCTGGGGACACGCTGTCCTCCCCCGAGTTCGACAGCGGTCCTTTCAGCTCCCAGTC
TGATGAGACCTCTCTCAGCACCACTGCCTCATCTGCCACGCCCACCAGTGAGCTGCTGCCCCTGGGTCCG
GTGGACGGCCGCTCCTGCTCCATGGACTCTGCCTACGGCACCCTCTCCCCAACCTCCTTACAAGACTTTG
TGGCCCCAGGCCCAATGGCAGAGCTAGTGCCTCGGGCCCCAGAGTCCCCACGAGTTCCTTCCCCTCCACC
CTCGCCCCGTCTCCGCCGCCGCACCCCTGTCCAGCTGTTGAGCTGCCCGCCCCACCTGCTCAAGTCTAAG
TCCGAGGCCAGCCTCCTCCAGCTGCTGGCAGGGGCTGGCACCCATGGGACACCCTCTGCCCCCAGCCGCA
GCCTGTCAGAGCTCTGCCTGGCTGTTCCAGCCCCAGGTATTAGGACTCAGGGCTCCCCTCAGGAAGCTGG
GCCCAGCTGGGATTGCCGAGGGGCCCCTAGCCCTGGCAGCGGTCCTGGGCTAGTCGGCTGCCTGGCCGGG

GAACCTGCAGGCTCCCACAGGAAGAGGTGTGGAGACCTGCCCTCGGGGGCCTCTCCCAGGGTCCAGCCTG
AGCCCCCACCAGGGGTCTCTGCCCAGCACAGGAAGCTGACCCTGGCCCAGCTCTACCGAATCAGGACCAC
CCTGCTGCTTAACTCCACGCTCACTGCCTCGGAGGTCTGAGCAGAGGGAGGCCCCCAAGAGTGCCATTGA
CCAAGAGACAGCAGACAGCCTGCCTCCTGGGGCGTGCCGGCACCTGCTTCAGCTACTGCCTCCTGTATGC
ATGAGCCGGATGCTGGGCAGGATCCCTGCCTACGCCCGGGCCCGATTTGCGCTTTGCCGGACTGGATGGA
GTGGAGGAGGCCCAGGCCACAGTACCACCCCACCTGCCCAGGCAGCCCCTCGTCACCTACTCCCCGAAGT
TACCAGCTCAGCTCGAGTCTTCAGGGCTGGGCTCCTAGGCTGCCCATCCTACTTCTACCCTCACTGGCCT
CCAGTGGGATTCACTCCTGCCCTGCCCCCACCTTCCCAGTCCCACAGGCCACCCCTGGCTTGGGCTGGGT
TCTGTGAAGTTACGTATTTATTGAGCTTTTGGTTCTTTTATAAAGACTTGTCTAGACTCC

>gi|8923495|ref|NM_017864.1| Homo sapiens hypothetical protein FLJ20530 (FLJ20530), mRNA
GAAAGGAAACATGGCTGCTTTTCTAAAGAATGTGTGTCTGGGGTTGGAAGATCTGCAGTATGTTTTCATG
ATTTCTTCACATGAGCTTTTCATTACATTGTTGAAAGATGAAGAACGAAAGCTACTTGTTGATCAGATGA
GGAAGAGATCCCCTAGAGTAAATCTGTGCATTAAACCTGTAACTTCATTTTATGATATCCCAGCTTCAGC
AAGTGTCAACATTGGTCAGTTAGAGCATCAACTTATATTGTCAGTGGATCCTTGGAGGATTAGACAAATT
TTAATTGAATTACATGGTATGACTTCAGAGCGCCAGTTCTGGACAGTGTCTAATAAGTGGGAAGTACCTT
CTGTCTATAGTGGTGTTATCCTGGGAATTAAAGACAATTTAACAAGAGATTTGGTTTATATTCTTATGGC
CAAAGGTTTGCACTGCAGTACTGTTAAGGACTTTTCCCATGCTAAACAGCTCTTTGCTGCTTGTTTGGAG
TTGGTAACAGAGTTCTCACCGAAGCTTCGTCAGGTCATGCTGAATGAGATGTTGCTTTTGGATATTCATA
CACACGAAGCTGGGACAGGGCAGGCAGGAGAGAGACCGCCATCCGACCTTATAAGTAGAGTACGAGGCTA
TCTGGAAATGAGGCTTCCTGATATTCCTCTTCGTCAAGTTATAGCTGAGGAATGTGTTGCCTTTATGTTA
AACTGGAGAGAAAATGAATACCTTACACTCCAAGTTCCTGCATTTTTGCTTCAGAGTAATCCATATGTAA
AGCTTGGACAGCTTTTAGCAGCTACATGCAAAGAACTTCCAGGCCCTAAAGAAAGTAGACGGACTGCCAA
AGACCTTTGGGAAGTTGTTGTTCAAATCTGTAGTGTGTCCAGTCAGCACAAACGAGGAAATGATGGCAGA
GTTAGTTTAATAAAACAGAGGGAATCTACGTTAGGTATCATGTATCGGAGTGAACTGCTTTCTTTTATCA
AAAAATTACGAGAACCACTCGTTTTGACTATTATTTTATCACTCTTTGCGAAACTTCACAATGTTCGGGA
GGACATTGTGAATGATATTACAGCTGAACACATTTCTATTTGGCCATCTTCCATTCCCAACCTCCAGTCT
GTGGACTTTGAAGCTGTGGCAATCACAGTGAAAGAGCTAGTTCGATATACACTCAGTATAAATCCAAATA
ACCATTCTTGGTTAATTATCCAGGCAGATATTTACTTTGCAACGAATCAGTATTCAGCAGCTCTTCATTA
TTACCTCCAGGCAGGAGCTGTGTGTTCTGACTTCTTTAACAAGGCTGTGCCCCCTGATGTTTATACAGAC
CAGGTAATAAAACGAATGATAAAATGTTGTTCTTTGCTGAATTGCCACACACAGGTGGCCATTTTATGTC
AGTTCCTCAGAGAAATTGACTACAAAACAGCGTTTAAATCTCTGCAAGAACAAAACAGTCATGATGCTAT
GGACTCCTACTACGACTACATATGGGATGTTACCATTTTGGAATACTTGACTTATCTTCATCATAAAAGA
GGAGAAACAGATAAAAGACAAATTGCAATCAAAGCCATCGGCCAGACAGAGTTGAATGCAAGCAATCCAG
AAGAAGTGTTACAGCTGGCAGCGCAGAGAAGGAAAAAAAAGTTTCTCCAAGCAATGGCAAAACTTTACTT
TTAAGCAGTTAAATTTTTTAACTTTTATTTTTTAAACAATGGGCTAAAAATAAACAGTATTAAAAGGTT
AAGTTTATATAAAAAAAAAAAAAAAAAA

>gi|4557600|ref|NM_000807.1| Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
CCTAGCGCTCCTCTCCGGCTTCCACCAGCCCATCGCTCCACGCTCTCTTGGCTGCTGCAGTCTCGGTCTC
TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCCAA
GTTTCCTATCTCGTCAAGATCAGGGCAAAAGAAGAAAACACCGAATTCTGCTTGCCGTTTCAGAGCGGCG
GTGATGAAGACAAAATTGAACATCTACAACATCGAGTTCCTGCTTTTTGTTTTCTTGGTGTGGGACCCTG
CCAGGTTGGTGCTGGCTAACATCCAAGAAGATGAGGCTAAAAATAACATTACCATCTTTACGAGAATTCT
TGACAGACTTCTGGATGGTTACGATAATCGGCTTAGACCAGGACTGGGAGACAGTATTACTGAAGTCTTC
ACTAACATCTACGTGACCAGTTTTGGCCCTGTCTCAGATACAGATATGGAATATACAATTGATGTTTTCT
TTCGACAAAAATGGAAAGATGAACGTTTAAAATTTAAAGGTCCTATGAATATCCTTCGACTAAACAATTT
AATGGCTAGCAAAATCTGGACTCCAGATACCTTTTTTCACAATGGGAAGAAATCAGTAGCTCATAATATG
ACAATGCCAAATAAGTTGCTTCGAATTCAGGATGATGGGACTCTGCTGTATACCATGAGGCTTACAGTTC
AAGCTGAATGCCCAATGCACTTGGAGGATTTCCCAATGGATGCTCATTCATGTCCTCTGAAATTTGGCAG
CTATGCATATACAACTTCAGAGGTCACTTATATTTGGACTTACAATGCATCTGATTCAGTACAGGTTGCT
CCTGATGGCTCTAGGTTAAATCAATATGACCTGCTGGGCCAATCAATCGGAAAGGAGACAATTAAATCCA
GTACAGGTGAATATACTGTAATGACAGCTCATTTCCACCTGAAAAGAAAAATTGGGTATTTTGTGATTCA
AACCTATCTGCCTTGCATCATGACTGTCATTCTCTCCCAAGTTTCATTCTGGCTTAACAGAGAATCTGTG
CCTGCAAGAACTGTGTTTGGAGTAACAACTGTCCTAACAATGACAACTCTAAGCATCAGTGCTCGGAATT

CTCTCCCCAAAGTGGCTTATGCAACTGCCATGGACTGGTTTATTGCTGTTTGTTATGCATTTGTGTTCTC
TGCCCTAATTGAATTTGCAACTGTTAATTACTTCACCAAAAGAGGATGGACTTGGGATGGAAGAGTGTA
GTAAATGACAAGAAAAAAGAAAAGGCTTCCGTTATGATACAGAACAACGCTTATGCAGTGGCTGTTGCCA
ATTATGCCCCGAATCTTTCAAAAGATCCAGTTCTCTCCACCATCTCCAAGAGTGCAACCACGCCAGAACC
CAACAAGAAGCCAGAAAACAAGCCAGCTGAAGCAAAGAAAACTTTCAACAGTGTTAGCAAAATTGACAGA
ATGTCCAGAATAGTTTTTCCAGTTTTGTTTGGTACCTTTAATTTAGTTTACTGGGCTACATATTTAAACA
GAGAACCTGTATTAGGGGTCAGTCCTTGAATTGAGACCCATGTTATCTTTGGGATGTATAGCAACATTAA
ATTTGGTTTGTTTTGCTATGTACAGTCTGACTAATAACTGCTAATTTGTGATCCAACATGTACAGTATGT
ATATAGTGACATAGCTTACCAGTAGACCTTTAATGGAGACATGCATTTGCTAACTCATGGAACTGCAGAC
AGAAAGCACTCCATGCGAAAACAGCCATTGCCTTTTTAAAGATTTACCCTAGGACCTGATTTAAAGTGA
ATTTCAAGTGACCTGATTAATTTCCTATTCTTCCAAATGAGATGAAAATGGGGATCCTGTACAACCCTTT
GTGGACCCTTTTGGTTTAGCTCTTAAGTAGGGGTATTTTCTACTGTTGCTTAATTATGATGGAAGATAAC
ATTGTCATTCCTAGATGAATCCTTTGAAGTAACAAACATTGTATCTGACATCAGCTCTGTTCATGAGTGC
TCAGAGTCCCTGCTAATGTAATTGGAAGCTTGGTACACATAAGAAAAACTAGAGATTTGAAATCTAGCTA
TGAATTACTCTATATAGTATCTATAGCCATGTACATATTACAGCATGACAAGCTCGAAATAATTATGAGT
CAGCCCGAAAGATGTTAAT

>gi|6031207|ref|NM_000810.2| Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 5 (GABRA5), mRNA
GAAGATGCTGTTGAGGGCCCTGGAGAAACTTCAGCAGAACAGGGCCTCTCCCCTTGCAGGCCGAGCCGGG
GCCCTGCGCCCTCCCCCTCCGCCCAGCTCGGCCAAGGGCGCATTTGCTGAGCGTCTGGCGGCCTCTACCG
GAGCACCTCTGCAGAGGGCCGATCCTCCAGCCCAGAGACGACATGTGGCGCTCGGGCGAGTGCCTTGCAG
AGAGAGGAGTAGCTTGCTGGCTTTGAACGCGTGGCGTGGCAGATATTTCAGAAAGCTTCAAGAACAAGCT
GGAGAAGGGAAGAGTTATTCCTCCATATTCACCTGCTTCAACTACTATTCTTATTGGGAATGGACAATGG
AATGTTCTCTGGTTTTATCATGATCAAAAACCTCCTTCTCTTTTGTATTTCCATGAACTTATCCAGTCAC
TTTGGCTTTTCACAGATGCCAACCAGTTCAGTGAAAGATGAGACCAATGACAACATCACGATATTTACCA
GGATCTTGGATGGGCTCTTGGATGGCTACGACAACAGACTTCGGCCCGGGCTGGGAGAGCGCATCACTCA
GGTGAGGACCGACATCTACGTCACCAGCTTCGGCCCGGTGTCCGACACGGAAATGGAGTACACCATAGAC
GTGTTTTTCCGACAAAGCTGGAAAGATGAAAGGCTTCGGTTTAAGGGGCCCATGCAGCGCCTCCCTCTCA
ACAACCTCCTTGCCAGCAAGATCTGGACCCCAGACACGTTCTTCCACAACGGGAAGAAGTCCATCGCTCA
CAACATGACCACGCCCAACAAGCTGCTGCGGCTGGAGGACGACGGCACCCTGCTCTACACCATGCGCTTG
ACCATCTCTGCAGAGTGCCCCATGCAGCTTGAGGACTTCCCGATGGATGCGCACGCTTGCCCTCTGAAAT
TTGGCAGCTATGCGTACCCTAATTCTGAAGTCGTTTACGTCTGGACCAACGGCTCCACCAAGTCGGTGGT
GGTGGCGGAAGATGGCTCCAGACTGAACCAGTACCACCTGATGGGGCAGACGGTGGGCACTGAGAACATC
AGCACCAGCACAGGCGAATACACAATCATGACAGCTCACTTCCACCTGAAAAGGAAGATTGGCTACTTTG
TCATCCAGACCTACCTTCCCTGCATAATGACCGTGATCTTATCACAGGTGTCCTTTTGGCTGAACCGGGA
ATCAGTCCCAGCCAGGACAGTTTTTGGGGTCACCACGGTGCTGACCATGACGACCCTCAGCATCAGCGCC
AGGAACTCTCTGCCCAAAGTGGCCTACGCCACCGCCATGGACTGGTTCATAGCTGTGTGCTATGCCTTCG
TCTTCTCGGCGCTGATAGAGTTTGCCACGGTCAATTACTTTACCAAGAGAGGCTGGGCCTGGGATGGCAA
AAAAGCCTTGGAAGCAGCCAAGATCAAGAAAAAGCGTGAAGTCATACTAAATAAGTCAACAAACGCTTTT
ACAACTGGGAAGATGTCTCACCCCCCAAACATTCCGAAGGAACAGACCCCAGCAGGGACGTCGAATACAA
CCTCAGTCTCAGTAAAACCCTCTGAAGAGAAGACTTCTGAAAGCAAAAAGACTTACAACAGTATCAGCAA
AATTGACAAAATGTCCCGAATCGTATTCCCAGTCTTGTTCGGCACTTTCAACTTAGTTTACTGGGCAACG
TATTTGAATAGGGAGCCGGTGATAAAAGGAGCCGCCTCTCCAAAATAACCGGCCACACTCCCAAACTCCA
AGACAGCCATACTTCCAGCGAAATGGTACCAAGGAGAGGTTTTGCTCACAGGGACTCTCCATATGTGAGC
ACTATCTTTCAGGAAATTTTTGCATGTTTAATAATATGTACAAATAATATTGCCTTGATGTTTCTATATG
TAACTTCAGATGTTTCCAAGATGTCCCATTGATAATTCGAGCAAACAACTTTCTGGAAAAACAGGATACG
ATGACTGACACTCAGATGCCCAGTATCATACGTTGATAGTTTACAAACAAGATACGTATATTTTTAACTG
CTTCAAGTGTTACCTAACAATGTTTTTTATACTTCAAATGTCATTTCATACAAATTTTCCCAGTGAATAA
ATATTTTAGGAAACTCTCCATGATTATTAGAAGACCAACTATATTGCGAGAAACAGAGATCATAAAGAGC
ACGTTTTCCATTATGAGGAAACTTGGACATTTATGTACAAAATGAATTGCCTTTGATAATTCTTACTGTT
CTGAAATTAGGAAAGTACTTGCATGATCTTACACGAAGAAATAGAATAGGCAAACTTTTATGTAGGCAGA
TTAATAACAGAAATACATCATATGTTAGATACACAAAATATT

>gi|4504018|ref|NM_000171.1| Homo sapiens glycine receptor, alpha 1 (startle disease/hyperekplexia, stiff man syndrome) (GLRA1), mRNA
CGGGAGGCAACAGACACGCTGGAGTTTAACAAACAGCAATACTCTTCGCGCTCCTGAAAAGCAGGTCTGG

ACGCTCTCCGTGGTGCTGAAACGCCTCGCAGCCGCCGCTGTCCGTGGTATCTACGACCCCCTCGCTCCAA
TTTCCCCTGGGGCTCTCCCTCCGCGCCCCTGTTCCCCGCCTCCCTTTAACATCTGGATTATTTTTTGCAA
TAGCGCTTTCTGGTTTTGTAAGTGCCAATTTGAAACATTTTTTGCCCCCATAACTCGTGGACTACAAAGC
ACAAAGGACCTGAAAAATGTACAGCTTCAATACTCTTCGACTCTACCTTTCGGGAGCCATTGTATTCTTC
AGCCTTGCTGCTTCTAAGGAGGCTGAAGCTGCTCGCTCCGCAACCAAGCCTATGTCACCCTCGGATTTCC
TGGATAAGCTAATGGGGAGAACCTCCGGATATGATGCCAGGATCAGGCCCAATTTTAAAGGTCCCCCAGT
GAACGTGAGCTGCAACATTTTCATCAACAGCTTTGGTTCCATTGCTGAGACAACCATGGACTATAGGGTC
AACATCTTCCTGCGGCAGCAATGGAACGACCCCCGCCTGGCCTATAATGAATACCCTGACGACTCTCTGG
ACCTGGACCCATCCATGCTGGACTCCATCTGGAAACCTGACCTGTTCTTTGCCAACGAGAAGGGGGCCCA
CTTCCATGAGATCACCACAGACAACAAATTGCTAAGGATCTCCCGGAATGGGAATGTCCTCTACAGCATC
AGAATCACCCTGACACTGGCCTGCCCCATGGACTTGAAGAATTTCCCCATGGATGTCCAGACATGTATCA
TGCAACTGGAAAGCTTTGGATATACGATGAATGACCTCATCTTTGAGTGGCAGGAACAGGGAGCCGTGCA
GGTAGCAGATGGACTAACTCTGCCCCAGTTTATCTTGAAGGAAGAGAAGGACTTGAGATACTGCACCAAG
CACTACAACACAGGTAAATTCACCTGCATTGAGGCCCGGTTCCACCTGGAGCGGCAGATGGGTTACTACC
TGATTCAGATGTATATTCCCAGCCTGCTCATTGTCATCCTCTCATGGATCTCCTTCTGGATCAACATGGA
TGCTGCACCTGCTCGTGTGGGCCTAGGCATCACCACTGTGCTCACCATGACCACCCAGAGCTCCGGCTCT
CGAGCATCTCTGCCCAAGGTGTCCTATGTGAAAGCCATTGACATTTGGATGGCAGTTTGCCTGCTCTTTG
TGTTCTCAGCCCTATTAGAATATGCTGCCGTTAACTTTGTGTCTCGGCAACATAAGGAGCTGCTCCGATT
CAGGAGGAAGCGGAGACATCACAAGGAGGATGAAGCTGGAGAAGGCCGCTTTAACTTCTCTGCCTATGGG
ATGGGCCCAGCCTGTCTACAGGCCAAGGATGGCATCTCAGTCAAGGGCGCCAACAACAGTAACACCACCA
ACCCCCCTCCTGCACCATCTAAGTCCCCAGAGGAGATGCGAAAACTCTTCATCCAGAGGGCCAAGAAGAT
CGACAAAATATCCCGCATTGGCTTCCCCATGGCCTTCCTCATTTTCAACATGTTCTACTGGATCATCTAC
AAGATTGTCCGTAGAGAGGACGTCCACAACCAGTGAAGGGTCTGAAAGGTTGGGGGAGGCTGGGAGAGGG
GAACGTGGGAATAGCACAGGAATCTGAGAGACGGT

>gi|20127456|ref|NM_004130.2| Homo sapiens glycogenin (GYG), mRNA
CTCTGAGTCACCAACCTGAGGCTGCCCCGGCCGCCTGCGCACCCGGCAGCACCATGACAGATCAGGCCTT
TGTGACACTAACCACAAACGATGCCTACGCCAAAGGTGCCCTGGTCCTGGGATCATCTCTGAAACAGCAC
AGGACCACCAGGAGGCTGGTCGTGCTCGCCACCCCTCAGGTCTCAGACTCCATGAGAAAAGTTTTAGAGA
CAGTCTTTGATGAAGTCATCATGGTAGATGTCTTGGACAGTGGCGATTCTGCTCATCTAACCTTAATGAA
GAGGCCAGAGTTGGGTGTCACGCTGACAAAGCTCCACTGCTGGTCGCTTACACAGTATTCAAAATGTGTA
TTCATGGATGCAGATACTCTGGTCCTAGCAAATATTGATGATCTTTTTGACAGAGAAGAATTGTCAGCAG
CACCAGACCCAGGGTGGCCTGACTGCTTCAATTCCGGAGTCTTCGTTTATCAGCCTTCAGTTGAAACATA
CAATCAGCTGTTGCATCTTGCTTCTGAGCAAGGTAGTTTTGATGGTGGGGACCAAGGCATACTGAACACA
TTTTTTAGCAGCTGGGCAACAACAGATATCAGAAAACACCTGCCGTTTATTTATAACCTAAGCAGCATCT
CTATATACTCCTACCTCCCGGCATTTAAAGTGTTTGGTGCAAGTGCCAAAGTTGTGCATTTCCTGGGACG
AGTCAAACCATGGAATTATACTTATGATCCCAAAACAAAAAGTGTCAAAAGTGAGGCCCATGATCCCAAC
ATGACTCATCCAGAGTTTCTCATCCTGTGGTGGAACATCTTTACCACCAACGTTTTACCTCTGCTTCAAC
AATTTGGCCTTGTCAAAGACACCTGCTCATATGTAAATGTGCTTTCAGACTTGGTCTATACACTGGCTTT
CTCTTGTGGCTTCTGTAGAAAGGAAGATGTCTCAGGAGCCATATCACATCTGTCCCTTGGGGAGATCCCA
GCTATGGCACAGCCGTTTGTATCCTCGGAAGAACGGAAGGAACGATGGGAACAGGGCCAGGCTGATTATA
TGGGAGCAGATTCCTTTGACAACATCAAGAGGAAACTTGACACTTACCTCCAGTAGAAACACTGCATTTT
TCTGTGAACACATCCACTTCACAAGCCTTGTTTCTGATACTTAGTATCTAGAGCTGGGTTGAGAAAAGTC
TGTTACAGTTGCTAGAGGTTTTCATTAAAACTTATCAGATGAGAGGCTTTTTTAGGATAAGAGGTGAGAA
CTGGGCAAAAGTTGTGAAGCAGCAATTCTGTTATATGGACAGTGTTCTGCTTTTTAATCCTATTTAGCTT
GTTTCAGAAATTCTCACTTTTGTTGACTGCCAACATACAAAGTAAGGGAAACTCAAGATATTAAGATGGC
TGTATCAGTTCTTAAAATCTGCAGAGCCTGGTTCAAAATCAGTCACTCCCTTCAGAAGCAGACATGGCAT
CTGTTCCTTGCTTGCTTGTTGGTTGTGTACCTTTCACGAGACCTGAATTTTAGAATTGCCCAGTGCTGCC
AGAGTGAGTGAGTGTAATTCTCCTTTCAGGTAAAGATAGGCTATCTCAACACTGCTGAGTGATTCATAAA
CATATCAACCAATAGCATTAACCCATTTTATTTCCTGTCCTTAGTGTCTGAAGATGCTCACCAGTTTTCT
GTGTACAGTAAGGCAGCATGCTAAAATGCTTTTGTTCAGTTCTGGATATTTGAAAATAGCAGTGTGTTCT
CTGATGGTTACCTGCAGTGGCACCCTGTACAAAAAATAAAAGACTTATTGGTGTAAA

>gi|5453673|ref|NM_003918.1| Homo sapiens glycogenin 2 (GYG2), mRNA
CGCGGGCTTGCGGGCAGGGGCTGCAGGGAGGAGGAGAGGACCCGCGCCCGCGGGGGCTGGGCGGAGGCGG
GGCCGGGCTTCCGGACAGAGGCCAATCGCTGCCCTCGGGGCCTCCAGCGCCGGCTCTGGGCCGAGGCAGC
CAGAGCGCGGAAGAGGCCTGGAAATCCACGCGGATTCCCGGAGACGGCGCCTCTGCTCTGCGGGTTCGTG

GCGAGGAAGTCCACCCACTGCTCCCGGGCGCAGGTCTGCAGGTCCGCGCCCACTGCCCGCGGCGCCACTG
ACCATGTCGGAGACAGAGTTTCACCATGGTGCCCAGGCTGGTCTCGAACTCCTGAGGTCAAGCAATTCAC
CCACCTCAGCCTCCCAAAGTGCTGGAATGACAGTGACTGATCAGGCTTTTGTCACACTAGCCACCAATGA
CATCTACTGCCAGGGCGCCCTGGTCCTGGGGCAGTCACTGAGGAGACACAGGCTGACGAGGAAGCTGGTG
GTGTTGATCACTCCTCAGGTGTCCAGCCTGCTCAGGGTCATCCTCTCGAAGGTGTTCGATGAAGTCATTG
AAGTGAATCTAATCGATAGTGCCGACTACATCCACCTGGCCTTTCTGAAGAGACCTGAGCTCGGGCTCAC
CCTCACCAAGCTTCACTGTTGGACTCTCACTCACTACAGCAAGTGTGTCTTCCTGGATGCAGACACTCTG
GTGCTGTCCAATGTCGATGAGCTGTTTGACAGGGGAGAGTTTTCTGCGGCCCCGGACCCCGGATGGCCGG
ATTGCTTCAATAGCGGGGTGTTTGTCTTCCAGCCTTCTCTCCACACGCATAAACTCCTGCTACAGCACGC
CATGGAACACGGCAGCTTTGACGGGGCAGACCAAGGCTTACTGAATAGTTTCTTCAGGAACTGGTCGACC
ACAGACATCCACAAGCACCTGCCGTTCATCTATAACTTGAGTAGTAACACGATGTACACTTACAGCCCTG
CCTTCAAGCAATTCGGTTCCAGTGCAAAGGTCGTCCACTTTTTGGGGTCCATGAAACCTTGGAACTACAA
GTACAATCCACAGAGTGGCTCGGTGTTGGAGCAAGGCTCAGTGTCCAGCAGCCAGCACCAGGCGGCATTC
CTTCATCTCTGGTGGACGGTCTACCAGAACAACGTGCTGCCCCTTTATAAAAGCGTCCAAGCGGGGGAAG
CACGCGCGTCTCCTGGTCACACACTTTGCCACAGTGATGTGGGGGGCCGTGTGCGGATTCAGCCTCTGG
TGTTGGAGAGCCGTGTGAAAATTCAACACCCAGTGCGGGCGTGCCGTGTGCAAATTCACCACTGGGTTCT
AACCAGCCTGCTCAGGGCCTTCCGGAGCCGACCCAGATAGTGGATGAGACCCTGTCCCTACCTGAAGGAC
GCCGTTCAGAAGATATGATAGCTTGTCCTGAAACTGAGACTCCTGCCGTGATAACGTGTGACCCACTGTC
CCAGCCTTCCCCTCAGCCTGCAGACTTCACAGAGACTGAAACCATCTTGCAGCCAGCAAATAAAGTCGAA
AGTGTCTCATCCGAGGAAACCTTCGAACCAAGCCAGGAACTCCCTGCTGAGGCTCTCAGGGACCCCAGTC
TGCAGGATGCACTGGAGGTCGACCTGGCCGTCTCTGTTTCCCAGATCTCCATCGAAGAGAAGGTGAAGGA
ATTGAGCCCCGAGGAAGAGAGGAGGAAGTGGGAGGAAGGCCGTATCGACTACATGGGGAAGGACGCGTTT
GCTCGCATCCAGGAGAAGCTGGACCGGTTCCTGCAGTAATCCGGCAGCTGGTGGGCGTTGTGTGTAGTTA
GACAATGTCCTGTTGGGTGGTCCTGTTGCGTGGAGATCTCCTCTGGTCCTTTCAAAGGGAAACGCTGTTG
AACCTTGTGCCTCTATTTATGCTTAATCCATTTGAGTGCCTCACACAAAAAACGTAGAGTATAGAAATCC
ACCTTAAAGCCCCTCGCCCCAACTTCTCCACCAACGCCTTCTGGGCTTTCTTCAGAGGTCACTTCTACCC
TTGAAGCTGTCGGCAAAAGCGAGCAGTAATAACATTCTAGTAGACTCTCGATGGTGGTCTCCGCTCTTGC
CCGAAGGACCTCTGAAGTACGCTGGATCTGTGTTGTACAGGTGCTGTGAGACCTACCCTATTCAGAATTA
AACCTCACTGCAAATTTCCTCCCATCACGAAGCTAACAACACTAATATACGTATTTAGCACCTCTGAGGC
TTTGCCATGGAGACCATTTCTGTAGGGCTAAGGAAACATTTAGACGTGGTGACTGACTTTCATTTGGACT
TGGCGAAGTGTATCTGAGAAACACCTCGGCTGTGGTCTCTCTGCTTTAAATCCTAACAGGACTTCCTAGA
GCGTTGACAGAAATTCTACTCGTGGACGTTGGGAAGAAAGATTGTAGGTGGCTTGGGGAATGTGGGTGGC
TTAGAGGATCTAAACCGATTCACTTCCTGGTTGAGAAGCAACGAGGGCTTGCTCTAAATCGTTTAGAGGA
TAACAGGATCTAGAGATGCTCTCTGCTTGACAACAAAAGTCAGGGTGCAGTCGGTCCACCCTTGACTGCT
CTTGGCTTGGTCTCTACCCTCACTACCTCAGTTCTCAATAACTTAGTGAATCACTGCCCTCCTCAAAGCC
ATTTCCACTCAGCTCTTTCCAGAGAATTCTCAGTTTTATGAGACGGGAAACTTTATTTCACGAGAAAGCC
TCATTGTCAGAAGTATCTTCATTCAATGGGCACAATATGCTGTGTATCTCACCAGGTAGCTGTCAGGGGC
CACCGAGAGTGTCGTTAAAAATGGGCATCGTTGTAATAAAGGAGGAAAGTGCGACTTTTGAAATGTTTGG
AAGGTTTATTTCTCATGCACATTCCAGGGAAAAGCAGAGAGTAAATTAGAGACGGGATAGGAAGGCCGTG
GGAGAACTCGATCCTAGCCTGTGTCAGCTGGATGTGTTTACGTGGAGAGGCGTGGCCACTTTTTAGGTCA
CCTGAAGCAGTTTAGCCTTTGGATAGAGGAACCTGCCTGAATTTATGGCATTAGTGGTGGCATTTTTTTG
TGTACAAGATGTGGGTGATGGAGGGGCTGTTTCTTTTTCCGTGTGGGTGGTTAATAATCGTCAGTCTCGG
AGGGCGATGCTCGTAGGATATTTCAGGTGAGTCAGGGTTGGATGGTCATCGGCTTTCAGAGGGAGACCAC
GGGAATGTTCAGGGAAACAATGTCAGCTTCTCTGAGGACCAGAATTC

>gi|30147854|ref|XM_301113.1| Homo sapiens similar to Glycogenin-1 (LOC350705), mRNA
ATGACAGATCAGGTCTTTGTGACACTGACCACAAATGATGCCTACACCAAAGGTGCCCTGGTCCTGGGCT
CATCTCTGAAACAGCACAGGACCACCAGAAGACTAGTCATGCTCGCCACCCCGCAGGTCTCAGACTCCAT
GAGAAAAGTTTTAGAGACAGTCTTTGATGAAATCATCGTGGTAGATGTCTTGGACAGTGGTGATTCTGCT
CATCTAACCTTAATGAAGAGGCCAGAGTTGGCATTTAAAGTGTTTGGTGCAAGTGCCAAAGTTGTGCATT
TCCTGGGACAAGTCAAACCATGGAATTATACTTATGATCCCAAAACAAAAAGTGTCAAAAATGAGTCCCA
CCATCCCAACGTGACTCATCCAGAGTTTCTCATCCTATGGTGGAACATCTTTACCACCACCGTTTTACCT
CTGCTTCAACAATTTGGCCTTGTCAAAGACACCTTCTCATACGTAAATGTGGAAAATGTCTCAGGAGCCA
TATCACATCTGTCCCTTGGGGGGATCCCAGCTATGGCACAGTCTGTGTATCCTCAGAAGAATGGAAGGAG
CGGTGGGAACAGGGCTAGACCGATTATATGGGAGCAGATTCCTTTGACAACATCAAGAGGAAGCTTGACA
CTTACCTCCAGTAGAAACACTGCATTTTCCTGTGGACACATCCACTTCACAAGCCTTGTTTCTGATACTT

AG

>gi|4757725|ref|NM_004641.1| Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 (MLLT10), mRNA
GCCCTCTTGATTATGTGTGCCCTCTCCGGGCGCCCGCGTTAGCGGCCGGGTGGAGGTGGGGAGGGAAGAC
GCTGAGGAGGAGGAGGAGGCGGAGGAGGCGGTGGAGGGGAGGTGGGGGGAATCAGCAAGGACATGGCTCC
TGACTCCTGTGCGGAACGTGAGTGACTGAGCGGCAAAGCCCGAATGGTCTCTAGCGACCGGCCCGTGTCA
CTGGAGGACGAGGTCTCCCATAGTATGAAGGAGATGATTGGAGGCTGTTGCGTTTGCTCAGACGAGAGAG
GCTGGGCCGAGAACCCGCTGGTTTATTGCGACGGGCACGGCTGCAGCGTCGCGGTGCATCAAGCTTGCTA
TGGCATTGTTCAAGTACCCACTGGACCGTGGTTTTGCAGGAAATGTGAATCTCAGGAGAGAGCAGCCAGA
GTGAGATGTGAACTTTGTCCCCATAAGGATGGAGCTTTAAAAAGAACAGATAATGGGGGTTGGGCCCATG
TGGTTTGTGCCCTGTATATTCCAGAGGTACAATTTGCCAATGTTTCCACAATGGAACCAATTGTTTTACA
GTCTGTTCCGCATGATCGTTATAATAAGACTTGCTACATTTGTGATGAACAAGGAAGAGAAAGCAAAGCA
GCCACTGGTGCTTGCATGACATGTAATAAACATGGATGTCGACAGGCTTTCCATGTAACATGCGCTCAGT
TTGCCGGACTGCTTTGTGAAGAAGAAGGTAATGGTGCCGATAATGTCCAATACTGTGGCTACTGTAAATA
CCATTTTAGTAAGCTGAAAAAGAGCAAACGGGGATCTAATAGGTCATATGATCAAAGTTTAAGTGATTCT
TCCTCTCACTCTCAGGATAAACATCATGAGAAAGAGAAAAAAAAATATAAAGAGAAGGACAAACACAAAC
AGAAACACAAGAAGCAGCCAGAACCATCACCTGCATTGGTTCCATCCTTGACTGTTACTACAGAAAAAAC
TTATACAAGCACTAGCAACAACTCTATATCTGGATCATTGAAGCGCTTGGAAGATACTACTGCACGATTT
ACAAATGCAAATTTCCAGGAAGTCTCTGCACACACCTCTAGTGGAAAAGATGTTTCAGAGACTAGAGGGT
CAGAGGGCAAAGGGAAGAAATCTTCAGCTCACAGCTCAGGTCAAAGGGGAAGAAAGCCTGGTGGTGGAAG
AAATCCAGGAACAACTGTGTCAGCAGCTAGCCCTTTTCCTCAAGGCAGTTTTTCAGGAACTCCAGGCAGT
GTAAAGTCATCTTCTGGAAGTTCAGTGCAGTCTCCCCAGGATTTCCTGAGCTTTACAGACTCAGATCTGC
GTAATGACAGTTACTCTCACTCCCAACAGTCATCAGCAACCAAAGATGTACATAAAGGAGAGTCTGGAAG
CCAGGAAGGGGGGGTAAATAGTTTTAGTACCTTAATTGGCCTCCCTTCAACCTCAGCTGTTACTTCACAG
CCTAAAAGCTTTGAAAATTCACCTGGAGATTTGGGTAATTCCAGCCTTCCTACAGCAGGATATAAGCGGG
CTCAAACTTCTGGCATAGAAGAAGAAACTGTAAAGGAAAAGAAAAGGAAAGGAAATAAACAAAGTAAGCA
TGGGCCTGGCAGACCCAAAGGAAACAAAAATCAAGAGAATGTTTCTCATCTCTCAGTTTCTTCTGCTTCA
CCAACATCATCTGTAGCATCAGCTGCAGGAAGCATAACAAGCTCTAGTCTGCAGAAATCTCCTACATTGC
TCAGGAATGGAAGTTTACAGAGCCTCAGTGTTGGCTCATCTCCAGTTGGTTCAGAAATTTCCATGCAGTA
TCGGCATGATGGAGCTTGCCCAACAACTACGTTCTCAGAGTTGCTGAATGCAATACACAACGACAGAGGT
GACAGTTCTACACTAACAAAGCAAGAACTTAAATTCATAGGTATTTATAACAGCAATGATGTAGCAGTAT
CGTTTCCAAATGTAGTATCTGGCTCGGGATCTAGTACTCCTGTCTCCAGCTCTCACTTACCTCAGCAGTC
TTCTGGGCATTTGCAACAAGTAGGAGCGCTCTCTCCCTCAGCTGTGTCATCTGCAGCCCCTGCTGTTGCT
ACAACTCAGGCAAATACTCTATCTGGATCTTCTCTCAGTCAGGCACCATCTCATATGTATGGCAATAGAT
CAAATTCATCAATGGCAGCTCTTATAGCTCAGTCTGAAAACAATCAAACAGATCAAGATCTTGGAGACAA
TAGCCGCAACCTAGTTGGCAGAGGAAGCTCACCCCGAGGAAGTCTCTCGCCACGATCCCCTGTAAGCAGC
TTACAGATTCGCTATGATCAACCAGGCAACAGCAGTTTGGAAAATCTGCCTCCAGTAGCAGCCAGCATAG
AACAGCTTTTGGAGAGGCAGTGGAGTGAAGGACAGCAATTTTTACTAGAACAGGGTACTCCTAGTGACAT
TTTAGGAATGCTGAAGTCATTACACCAACTTCAAGTTGAAAACCGAAGATTAGAGGAACAAATTAAAAAC
TTGACTGCCAAAAAGGAACGGCTTCAGTTATTGAATGCACAGCTTTCAGTGCCTTTTCCAACAATAACAG
CAAATCCTAGTCCGTCTCATCAAATACACACATTTTCAGCACAGACTGCTCCTACTACTGATTCCTTGAA
CAGCAGTAAGAGCCCTCATATAGGAAACAGCTTTTTACCTGATAATTCTCTTCCTGTATTAAATCAGGAC
TTAACCTCCAGTGGACAAAGTACCAGCAGCTCATCAGCTCTTTCTACCCCACCTCCTGCTGGGCAGAGTC
CGGCTCAACAAGGCTCAGGAGTGAGTGGAGTTCAGCAGGTCAATGGCGTGACAGTGGGGGCACTAGCTAG
TGGAATGCAGCCTGTAACTTCCACCATTCCTGCCGTGTCTGCAGTGGGTGGAATAATTGGAGCTTTGCCA
GGTAACCAACTGGCAATTAATGGCATTGTAGGAGCTTTAAATGGGGTTATGCAGACTCCTGTCACAATGT
CCCAGAACCCTACCCCTCTCACCCACACAACCGTACCACCTAATGCAACACATCCAATGCCAGCTACACT
GACTAACAGTGCCTCAGGACTAGGATTACTTTCTGACCAGCAACGACAAATACTTATTCATCAACAGCAG
TTTCAGCAGTTGTTAAATTCTCAACAGCTCACACCAGTACACAGGCACCCCCACTTCACACAGCTACCAC
CAACCCATTTCTCACCATCCATGGAGATAATGCAAGTCAGAAAGTAGCAAGACTTAGTGATAAAACTGGG
CCTGTAGCTCAAGAGAAAAGTTGACACCTGAGAAACATCTAGAAATTGCCTATCCTGCTGTTCTAGCACT
TCATCTGGCTGCCTTTGCAGTCCTTTTACTACAGCTATGAAGAAACGCAACAAGAAACTCAATGCACAAC
AAAGGATTAATTGCTGCAAGGACATTCTTGTAAGGCTTTGATTAGTTTTCTTGTTGCTTTGTTGCACTGA
AATGGAATTCCCATGCCCCTACCCCTTACCCCAGTTTTTTGAACATGGAAAGAAAATTTAATAACTTTTT
AAAGTGACATAATTTACATGCAATATGTTTATCAACTCAAGAATTTAATATAGTTGGTACACAACTAGTT

TTGTTTATAAATTGGAGATGCAAATAGCAAAACTAAATACTTGCTCCATTTACAAACTACTTGATTTTAT
TGTACAAGTTGAAATATGCTCTTTTGTTTGGGTTACAGTATGCTTGCTCTAAGTCAAATTCCAAGGAACT
AATTTCTTCTCCTGGAGTTGCATTGATTCAGTATTACAAATATATAGCACATCACCTGGGAC

>gi|5174576|ref|NM_005937.1| Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 (MLLT6), mRNA
ATGAAGGAGATGGTAGGAGGCTGCTGCGTATGTTCGGACGAGAGGGGCTGGGCCGAGAACCCGCTGGTCT
ACTGCGATGGGCACGCGTGCAGCGTGGCCGTCCACCAAGCTTGCTATGGCATCGTTCAGGTGCCAACGGG
ACCCTGGTTCTGCCGGAAATGTGAATCTCAGGAGCGAGCAGCCAGGGTGAGGTGTGAGCTGTGCCCACAC
AAAGACGGGGCATTGAAGAGGACTGATAATGGAGGCTGGGCACACGTGGTGTGTGCCCTCTACATCCCCG
AGGTGCAATTTGCCAACGTGCTCACCATGGAGCCCATCGTGCTGCAGTACGTGCCTCATGATCGCTTCAA
CAAGACCTGTTACATCTGCGAGGAGACGGGCCGGGAGAGCAAGGCGGCCTCGGGAGCCTGCATGACCTGT
AACCGCCATGGATGTCGACAAGCTTTCCACGTCACCTGTGCCCAAATGGCAGGCTTGCTGTGTGAGGAAG
AAGTGCTGGAGGTGGACAACGTCAAGTACTGCGGCTACTGCAAATACCACTTCAGCAAGATGAAGACATC
CCGGCACAGCAGCGGGGGAGGCGGAGGAGGCGCTGGAGGAGGAGGTGGCAGCATGGGGGGAGGTGGCAGT
GGTTTCATCTCTGGGAGGAGAAGCCGGTCAGCCTCACCATCCACGCAGCAGGAGAAGCACCCCACCCACC
ACGAGAGGGGCCAGAAGAAGAGTCGAAAGGACAAAGAACGCCTTAAGCAGAAGCACAAGAAGCGGCCTGA
GTCGCCCCCCAGCATCCTCACCCCGCCCGTGGTCCCCACTGCTGACAAGGTCTCCTCCTCGGCTTCCTCT
TCCTCCCACCACGAGGCCAGCACGCAGGAGACCTCTGAGAGCAGCAGGGAGTCAAAGGGGAAAAAGTCTT
CCAGCCATAGCCTGAGTCATAAAGGGAAGAAACTGAGCAGTGGGAAAGGTGTGAGCAGTTTTACCTCCGC
CTCCTCTTCTTCCTCCTCCTCTTCCTCCTCCTCTGGGGGGCCCTTCCAGCCTGCAGTCTCGTCCCTGCAG
AGCTCCCCTGACTTCTCTGCATTCCCCAAGCTGGAGCAGCCAGAGGAGGACAAGTACTCCAAGCCCACAG
CCCCCGCCCCTTCAGCCCCTCCTTCTCCCTCAGCTCCCGAGCCCCCCAAGGCTGACCTTTTTGAGCAGAA
GGTGGTCTTCTCTGGCTTTGGGCCCATCATGCGCTTCTCCACCACCACCTCCAGCTCAGGCCGGGCCCGG
GCGCCCTCCCCTGGGGACTATAAGTCTCCCCACGTCACGGGGTCTGGGGCCTCGGCAGGCACCCACAAAC
GGATGCCCGCACTGAGTGCCACCCCTGTGCCTGCTGATGAGACCCCTGAGACAGGCCTGAAGGAGAAGAA
GCACAAAGCCAGCAAGAGGAGCCGCCATGGGCCAGGCCGTCCCAAGGGCAGCCGGAACAAGGAGGGCACT
GGGGGCCCAGCTGCCCCATCCTTGCCCAGTGCCCAGCTGGCTGGCTTTACCGCCACTGCTGCCTCACCCT
TCTCTGGAGGTTCCCTGGTCAGCTCCGGCCTGGGAGGTCTGTCCTCCCGAACCTTTGGGCCTTCTGGGAG
CTTGCCCAGCTTGAGCCTGGAGTCCCCCTTACTAGGGGCAGGCATCTACACCAGTAATAAGGACCCCATC
TCCCACAGTGGCGGGATGCTGCGGGCTGTCTGCAGCACCCCTCTCTCCTCCAGCCTCCTGGGGCCCCCAG
GGACCTCGGCCCTGCCCCGCCTCAGCCGCTCCCCGTTCACCAGCACCCTCCCCTCCTCTTCTGCTTCTAT
CTCCACCACTCAGGTGTTTTCTCTGGCTGGCTCTACCTTTAGCCTCCCTTCTACCCACATCTTTGGAACC
CCCATGGGTGCCGTTAATCCCCTCCTCTCCCAAGCTGAGAGCAGCCACACAGAGCCAGACCTGGAGGACT
GCAGCTTCCGGTGTCGGGGGACCTCCCCTCAGGAGAGTCTGTCTTCCATGTCCCCCATCAGCAGCCTCCC
CGCACTCTTCGACCAGACAGCCTCTGCACCCTGTGGGGGCGGCCAGTTAGACCCGGCGGCCCCAGGGACG
ACTAACATGGAGCAGCTTCTGGAGAAGCAGGGCGACGGGGAGGCCGGCGTCAACATCGTGGAGATGCTGA
AGGCGCTGCACGCGCTGCAGAAGGAGAACCAGCGGCTGCAAGAGCAGATCCTGAGCCTGACGGCCAAAAA
GGAGCGGCTGCAGATTCTCAACGTGCAGCTCTCTGTGCCCTTCCCTGCCCTGCCTGCTGCCCTGCCTGCC
GCCAACGGCCCTGTCCCTGGGCCCTATGGCCTGCCTCCCCAAGCCGGGAGCAGCGACTCCTTGAGCACCA
GCAAGAGCCCTCCGGGAAAGAGCAGCCTCGGCCTGGACAACTCGCTGTCCACTTCTTCTGAGGACCCACA
CTCAGGCTGCCCGAGCCGCAGCAGCTCGTCGCTGTCCTTCCACAGCACGCCCCCACCGCTGCCCCTCCTC
CAGCAGAGCCCTGCCACTCTGCCCCTGGCCCTGCCTGGGGCCCCTGCCCCACTCCCGCCCCAGCCGCAGA
ACGGGTTGGGCCGGGCACCCGGGGCAGCGGGGCTGGGGGCCATGCCCATGGCTGAGGGGCTGTTGGGGGG
GCTGGCAGGCAGTGGGGGCCTGCCCCTCAATGGGCTCCTTGGGGGGTTGAATGGGGCCGCTGCCCCCAAC
CCCGCAAGCTTGAGCCAGGCTGGCGGGGCCCCCACGCTGCAGCTGCCAGGCTGTCTCAACAGCCTTACAG
AGCAGCAGAGACATCTCCTTCAGCAGCAAGAGCAGCAGCTCCAGCAACTCCAGCAGCTCCTGGCCTCCCC
GCAGCTGACCCCGGAACACCAGACTGTTGTCTACCAGATGATCCAGCAGATCCAGCAGAAACGGGAGCTG
CAGCGTCTGCAGATGGCTGGGGGCTCCCAGCTGCCCATGGCCAGCCTGCTGGCAGGAAGCTCCACCCCGC
TGCTGTCTGCGGGTACCCCTGGCCTGCTGCCCACAGCGTCTGCTCCACCCCTGCTGCCCGCTGGAGCCCT
AGTGGCTCCCTCGCTTGGCAACAACACAAGTCTCATGGCCGCAGCAGCTGCAGCTGCAGCAGTAGCAGCA
GCAGGCGGACCTCCAGTCCTCACTGCCCAGACCAACCCCTTCCTCAGCCTGTCGGGAGCAGAGGGCAGTG
GCGGTGGCCCCAAAGGAGGGACCGCTGACAAAGGAGCCTCAGCCAACCAGGAAAAAGGCTAA

>gi|4505956|ref|NM_002697.1| Homo sapiens POU domain, class 2, transcription factor 1 (POU2F1), mRNA

GAGGAGCAGCGAGTCAAGATGAGAGTTCAGCCGCGGCGGCAGCAGCAGCAGACTCAAGAATGAACAATCC
GTCAGAAACCAGTAAACCATCTATGGAGAGTGGAGATGGCAACACAGGCACACAAACCAATGGTCTGGAC
TTTCAGAAGCAGCCTGTGCCTGTAGGAGGAGCAATCTCAACAGCCCAGGCGCAGGCTTTCCTTGGACATC
TCCATCAGGTCCAACTCGCTGGAACAAGTTTACAGGCTGCTGCTCAGTCTTTAAATGTACAGTCTAAATC
TAATGAAGAATCGGGGGATTCGCAGCAGCCAAGCCAGCCTTCCCAGCAGCCTTCAGTGCAGGCAGCCATT
CCCCAGACCCAGCTTATGCTAGCTGGAGGACAGATAACTGGGCTTACTTTGACGCCTGCCCAGCAACAGT
TACTACTCCAGCAGGCACAGGCACAGGCACAGCTGCTGGCTGCTGCAGTGCAGCAGCACTCCGCCAGCCA
GCAGCACAGTGCTGCTGGAGCCACCATCTCCGCCTCTGCTGCCACGCCCATGACGCAGATCCCCCTGTCT
CAGCCCATACAGATCGCACAGGATCTTCAACAACTGCAACAGCTTCAACAGCAGAATCTCAACCTGCAAC
AGTTTGTGTTGGTGCATCCAACCACCAATTTGCAGCCAGCGCAGTTTATCATCTCACAGACGCCCCAGGG
CCAGCAGGGTCTCCTGCAAGCGCAAAATCTTCAAACGCAACTACCTCAGCAAAGCCAAGCCAACCTCCTA
CAGTCGCAGCCAAGCATCACCCTCACCTCCCAGCCAGCAACCCCAACACGCACAATAGCAGCAACCCCAA
TTCAGACACTTCCACAGAGCCAGTCAACACCAAAGCGAATTGATACTCCCAGCTTGGAGGAGCCCAGTGA
CCTTGAGGAGCTTGAGCAGTTTGCCAAGACCTTCAAACAAAGACGAATCAAACTTGGATTCACTCAGGGT
GATGTTGGGCTCGCTATGGGGAAACTATATGGAAATGACTTCAGCCAAACTACCATCTCTCGATTTGAAG
CCTTGAACCTCAGCTTTAAGAACATGTGCAAGTTGAAGCCACTTTTAGAGAAGTGGCTAAATGATGCAGA
GAACCTCTCATCTGATTCGTCCCTCTCCAGCCCAAGTGCCCTGAATTCTCCAGGAATTGAGGGCTTGAGC
CGTAGGAGGAAGAAACGCACCAGCATAGAGACCAACATCCGTGTGGCCTTAGAGAAGAGTTTCTTGGAGA
ATCAAAAGCCTACCTCGGAAGAGATCACTATGATTGCTGATCAGCTCAATATGGAAAAAGAGGTGATTCG
TGTTTGGTTCTGTAACCGCCGCCAGAAAGAAAAAAGAATCAACCCACCAAGCAGTGGTGGGACCAGCAGC
TCACCTATTAAAGCAATTTTCCCCAGCCCAACTTCACTGGTGGCGACCACACCAAGCCTTGTGACTAGCA
GTGCAGCAACTACCCTCACAGTCAGCCCTGTCCTCCCTCTGACCAGTGCTGCTGTGACGAATCTTTCAGT
TACAGGCACTTCAGACACCACCTCCAACAACACAGCAACCGTGATTTCCACAGCGCCTCCAGCTTCCTCA
GCAGTCACGTCCCCCTCTCTGAGTCCCTCCCCTTCTGCCTCAGCCTCCACCTCCGAGGCATCCAGTGCCA
GTGAGACCAGCACAACACAGACCACCTCCACTCCTTTGTCCTCCCCTCTTGGGACCAGCCAGGTGATGGT
GACAGCATCAGGTTTGCAAACAGCAGCAGCTGCTGCCCTTCAAGGAGCTGCACAGTTGCCAGCAAATGCC
AGTCTTGCTGCCATGGCAGCTGCTGCAGGACTAAACCCAAGCCTGATGGCACCCTCACAGTTTGCGGCTG
GAGGTGCCTTACTCAGTCTGAATCCAGGGACCCTGAGCGGTGCTCTCAGCCCAGCTCTAATGAGCAACAG
TACACTGGCAACTATTCAAGCTCTTGCTTCTGGTGGCTCTCTTCCAATAACATCACTTGATGCAACTGGG
AACCTGGTATTTGCCAATGCGGGAGGAGCCCCCAACATCGTGACTGCCCCTCTGTTCCTGAACCCTCAGA
ACCTCTCTCTGCTCACCAGCAACCCTGTTAGCTTGGTCTCTGCCGCCGCAGCATCTGCAGGGAACTCTGC
ACCTGTAGCCAGCCTTCACGCCACCTCCACCTCTGCTGAGTCCATCCAGAACTCTCTCTTCACAGTGGCC
TCTGCCAGCGGGGCTGCGTCCACCACCACCACCGCCTCCAAGGCACAGTGAGCTGGGCAGAGCTGGGCTG
CCAGAAGCCTTTTTCACTCTGCAGTGTGATTGGACTGCCAGCCAGGTTAATAAACTGAAAAATGTGATTG
GCTTCCTCTCGCCGTGTTGTGAGGGCAAAGGAGAGAAGGGAGAAAAAAAAAAAAAAAACCACACACACCC
ATACACAATATACCAGAAAAGGAAGGAAGGATGGAGACGGAACATTTGCCTAATTTGTAATAAAACACTG
TCTTTTCAGGGTTGCTTCATGGGTTGGAGGACTTTCTAACCAAAAATTAAAAAAAAAAAAAAA

>gi|4505958|ref|NM_002698.1| Homo sapiens POU domain, class 2, transcription factor 2 (POU2F2), mRNA
CGTCAACATGAGTTGGGCCTGGGGCAGATGAGGCTGGCTGGCGGGGCGGGCAGCATGGTTCACTCCAGCA
TGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAGGCCGAGAAGCAAGGTCTGGACTCCCCATCAGA
GCACACAGACACCGAAAGAAATGGACCAGACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTC
TCCGTGTCCCCAACTGGCCCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTCAGCCCCAGCAG
CACCCCTGCCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAGCT
AGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGTGCCAGGCCACCACCTCCAGCCA
CCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTGCTACCGACACCAAATCTATTCC
AGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCCCAGCCCCGGGCCGGGCTTCCCACACAGCCCCC
CAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGTGATCTGGAGGAGCTGGAGCAATTCGCCCGC
ACCTTCAAGCAACGCCGCATCAAGCTGGGCTTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCT
ACGGCAACGACTTCAGCCAGACGACCATTTCCCGCTTCGAGGCCCTCAACCTGAGCTTCAAGAACATGTG
CAAACTCAAGCCCCTCCTGGAGAAGTGGCTCAACGATGCAGAGACTATGTCTGTGGACTCAAGCCTGCCC
AGCCCCAACCAGCTGAGCAGCCCCAGCCTGGGTTTCGACGGCCTGCCCGGCCGGAGACGCAAGAAGAGGA
CCAGCATCGAGACAAACGTCCGCTTCGCCTTAGAGAAGAGTTTTCTAGCGAACCAGAAGCCTACCTCAGA
GGAGATCCTGCTGATCGCCGAGCAGCTGCACATGGAGAAGGAAGTGATCCGCGTCTGGTTCTGCAACCGG
CGCCAGAAGGAGAAACGCATCAACCCCTGCAGTGCGGCCCCCATGCTGCCCAGCCCAGGGAAGCCGGCCA
GCTACAGCCCCCATATGGTCACACCCCAAGGGGGCGCGGGGACCTTACCGTTGTCCCAAGCTTCCAGCAG

TCTGAGCACAACAGTTACTACCTTATCCTCAGCTGTGGGGACGCTCCACCCCAGCCGGACAGCTGGAGGG
GGTGGGGGCGGGGGCGGGGCTGCGCCCCCCCTCAATTCCATCCCCTCTGTCACTCCCCCACCCCCGGCCA
CCACCAACAGCACAAACCCCAGCCCTCAAGGCAGCCACTCGGCTATCGGCTTGTCAGGCCTGAACCCCAG
CACGGGCCCTGGCCTCTGGTGGAACCCTGCCCCTTACCAGCCTTGATGGCAGCGGGAATCTGGTGCTGGG
GGCAGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTTGAATCATGCTGGGCTG
CCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGCTGTGGCAGCCTCCATCT
CCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTCATCCTCCTCCTCCTCCACTTGCAGCGA
GACGGCAGCACAGACCCCTGGAGGTCCAGGGGGGCCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCC
ATGCCTCCCCTCCCATTCCTCTGGTCCCTGCCTTGGTCCCTTGCCTGGGAAGAGGGGCAGGAGGCCAGTG
GTGGGGACGCAGAGGGTCCTCAGAGCAGGAGTGACAAGGGAGGAAAGACCAAAAAAACAACCAACCAAAA
AAAAAAAAAAAAAAGGAAAGAAACTAACCAACAAAAGAGAAAACCAAAAATAATCACAACAGAAACCAGC
TGCCCCAAAGGAACCAGAGGTGAAAAACAAACAAAAAAAACCAAAAACAAACCAAAAAAAAAAAAAAACC
TCTACCCCCTCTAGAGCC

>gi|7657408|ref|NM_014352.1| Homo sapiens POU domain, class 2, transcription factor 3 (POU2F3), mRNA
GGGGAGGATGGTGAATCTGGAGTCCATGCACACAGATATCAAGATGAGTGGGGATGTAGCCGATTCCACG
GATGCTCGCAGCACTCTCAGCCAGGTGGAGCCAGGAAATGATCGAAAAGGCCTAGATTTCAACAGGCAGA
TTAAAACCGAAGATCTCAGTGACTCCCTGCAGCAGACCCTCTCCCATCGGCCATGCCACCTGAGTCAAGG
ACCTGCCATGATGTCCGGAAACCAAATGTCTGGGCTAAATGCCAGCCCATGTCAGGACATGGCTTCCCTC
CATCCGCTCCAGCAGCTTGTGCTGGTTCCCGGCCACTTACAGTCTGTATCCCAGTTCCTGCTATCTCAGA
CCCAGCCTGGGCAGCAAGGTCTGCAGCCAAATCTCCTCCCCTTTCCACAGCAACAAAGCGGTCTCCTCCT
CCCACAGACTGGGCCGGGACTGGCATCCCAGGCATTTGGGCACCCTGGGCTGCCAGGATCCTCTTTAGAA
CCCCACCTGGAAGCATCCCAGCATCTCCCAGTGCCCAAGCATCTACCCAGCTCTGGAGGGGCCGATGAGC
CCAGTGACCTCGAGGAGCTGGAGAAGTTTGCCAAGACCTTCAAGCAGAGGCGCATTAAGCTGGGCTTCAC
ACAGGGAGATGTGGGGCTGGCGATGGGAAAGCTGTATGGCAACGACTTCAGCCAGACCACCATCTCACGA
TTTGAGGCCCTCAACCTGAGCTTCAAGAACATGTGCAAGCTCAAGCCCCTGCTGGAGAAGTGGCTGAATG
ATGCAGAGTCCTCTCCGTCAGACCCCTCAGTGAGCACGCCCAGCTCCTACCCCAGCCTCAGTGAAGTATT
TGGTAGGAAGAGAAAGAAACGGACCAGCATCGAGACCAACATCCGCCTGACTCTGGAGAAGAGGTTTCAA
GATAACCCAAAACCCAGCTCGGAGGAGATCTCCATGATTGCAGAGCAGTTGTCCATGGAGAAGGAGGTGG
TGAGGGTCTGGTTCTGCAACCGACGCCAAAAGGAGAAGCGAATCAACTGCCCTGTGGCCACACCCATCAA
ACCACCTGTCTACAACTCCCGGCTGGTATCTCCCTCAGGGTCTCTGGGCCCCCTCTCTGTCCCTCCTGTC
CACAGTACCATGCCTGGAACAGTAACGTCATCCTGTTCCCCTGGGAACAACAGCAGGCCTTCATCTCCTG
GCTCAGGACTCCACGCCAGCAGCCCCACTGCATCTCAAAATAACTCCAAAGCAGCAGTGAACTCCGCCTC
CAGTTTTAACTCTTCAGGATCTTGGTACCGATGGAATCATTCCACCTACCTCCACTGAGACCAAAAAGTT
TCTCCTACTCCAGCTGGCCCTGTATTCCCCTGGAAGGAAGGGAATCATGCCTTCTATATACAGACAGATT
GCCTTCAGAAGAGTGGAAGAAAATCTCCACTATCAATGAACCCAGACTCTTGTCTTCTTCAAGAGCAAGG
GCCTCCGGAGATCCAAACTGTGATTGAACCAAGTGCAGACTCCTAATGCTCTTGAAATACACAGCCCCTC
CTAGGAGCTTACCATTTTCACCTTCCTTGCCTATGCCCTTGCCTTCTAGTTCCAAATATTTTAGCCAGCT
TCACTGTGGCAATAGTCTTTCAGAGAAAAGACTTCTTGCTGTTATTCTCCAACTCATCCGTGGGCTTCTG
GGGACAGCCATTTGGCTGGGGTGCCAAACACCAGAAGGGGAGATAATAGTTTTGACTCTGAACTTGGCCA
CAACCCCTGAACTGATCCCAAAATCTGTGAAAAGATTTGAATCTGATATCTCCACCAAAGCCTTGATGTT
TTCTCTGTACAGCTAAGTTTTCTGATGGAATCTTCATCTCACCCCATTTTCTTTTTAACCTCGCCCCCTT
TTCTACAATCAAATCCATTCATTATTGCGCCCTCCAGGTCCCCTCCTTTTTGCAGAAGGTGTAAAAGAGC
TGCCCTTGGTGGGTGCCCTTGAGCATGTTGCAACGCCTGCTGGTGCCCTTCTGTCTGTCCACGTCTGCCT
AGGGCTCAGGAGTGCTTGTTCTTTCCCTGGCGCCCTGGGTTTCTCTTTATCCTGTCCCCTCTCCTTTCTC
CTGGCAGCAGAAAAGGAAGAACACAAGAGCAAACACACAACAATGATGGTGGCAAAGTACCTGTATATAG
CCCTTTCCCATTTTTGCATTATGTTCTTAACTCCTTAATGTGGAATTTTCCAGCAAAATGTTTAACTCAG
GTGTGATTTTTGAAAATGTCTCTGTAATATTTTATCTTCTTTAAAAAAAAGGGGGGGAAATACCAAAGTG
TGAAATACTGTGCTACCTTCCAGAGTTCCCACATGGGCTGGGATTTTTTTTTCTTTTTCTTTTTTTTTTT
TTTTTTTGAGACAGTCTTGCTCCAGCCCAGGCTGGAGTGCAGTGGCATGATCTTGGCTCACTGCATGCTC
TGCCACTTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTCAAGTAGCGGATTACAGGCGCCCACCACCAA
AAATTAGCCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGTCAGGCTGGTCTTG
AACTCCTGACCTCCTGATCCACCCACCTCAGCGTCCCGAAGTGCTGGGATTACAGGTGTGAGCCACCGCG
CCTGGCCTGGGCTGGGAATCTTTGTTGACTTCTTTGGGAACATTATCTCTAGAGTCTGCTTTTTTGTGGG
CCAGTTTGTAGAGATGTAACATGAAGCCATTCCAGAAATGGTAACTTAAAAAAAAAAAGACTACATGTCT
AGGAAACTGTTGAGATTCAAAGGAATCTCACTGTTCCTAAATAAATGTGTATAGTGATTATGAAAAGT

>gi|31543438|ref|NM_002740.2| Homo sapiens protein kinase C, iota (PRKCI), mRNA
AGCGGTTTTGGGCCCGGGCGGCTGTAGAGGCGGCGGCGCCTACGGGCAGTGGGAGGAGCCGCGCGGTTCC
GGCTGCTCCGGCGAGGCGACCCTTGGGTCGGCGCTGCGGGCGAGGTGGGCAGGTAGGTGGGCGGACGGCC
GCGGTTCTCCGGCAAGCGCAGGCGGCGGAGTCCCCCACGGCGCCCGAAGCGCCCCCCCGCACCCCCGGCC
TCCAGCGTTGAGGCGGGGGAGTGAGGAGATGCCGACCCAGAGGGACAGCAGCACCATGTCCCACACGGTC
GCAGGCGGCGGCAGCGGGGACCATTCCCACCAGGTCCGGGTGAAAGCCTACTACCGCGGGGATATCATGA
TAACACATTTTGAACCTTCCATCTCCTTTGAGGGCCTTTGCAATGAGGTTCGAGACATGTGTTCTTTTGA
CAACGAACAGCTCTTCACCATGAAATGGATAGATGAGGAAGGAGACCCGTGTACAGTATCATCTCAGTTG
GAGTTAGAAGAAGCCTTTAGACTTTATGAGCTAAACAAGGATTCTGAACTCTTGATTCATGTGTTCCCTT
GTGTACCAGAACGTCCTGGGATGCCTTGTCCAGGAGAAGATAAATCCATCTACCGTAGAGGTGCACGCCG
CTGGAGAAAGCTTTATTGTGCCAATGGCCACACTTTCCAAGCCAAGCGTTTCAACAGGCGTGCTCACTGT
GCCATCTGCACAGACCGAATATGGGGACTTGGACGCCAAGGATATAAGTGCATCAACTGCAAACTCTTGG
TTCATAAGAAGTGCCATAAACTCGTCACAATTGAATGTGGGCGGCATTCTTTGCCACAGGAACCAGTGAT
GCCCATGGATCAGTCATCCATGCATTCTGACCATGCACAGACAGTAATTCCATATAATCCTTCAAGTCAT
GAGAGTTTGGATCAAGTTGGTGAAGAAAAAGAGGCAATGAACACCAGGGAAAGTGGCAAAGCTTCATCCA
GTCTAGGTCTTCAGGATTTTGATTTGCTCCGGGTAATAGGAAGAGGAAGTTATGCCAAAGTACTGTTGGT
TCGATTAAAAAAAACAGATCGTATTTATGCAATGAAAGTTGTGAAAAAAGAGCTTGTTAATGATGATGAG
GATATTGATTGGGTACAGACAGAGAAGCATGTGTTTGAGCAGGCATCCAATCATCCTTTCCTTGTTGGGC
TGCATTCTTGCTTTCAGACAGAAAGCAGATTGTTCTTTGTTATAGAGTATGTAAATGGAGGAGACCTAAT
GTTTCATATGCAGCGACAAAGAAAACTTCCTGAAGAACATGCCAGATTTTACTCTGCAGAAATCAGTCTA
GCATTAAATTATCTTCATGAGCGAGGGATAATTTATAGAGATTTGAAACTGGACAATGTATTACTGGACT
CTGAAGGCCACATTAAACTCACTGACTACGGCATGTGTAAGGAAGGATTACGGCCAGGAGATACAACCAG
CACTTTCTGTGGTACTCCTAATTACATTGCTCCTGAAATTTTAAGAGGAGAAGATTATGGTTTCAGTGTT
GACTGGTGGGCTCTTGGAGTGCTCATGTTTGAGATGATGGCAGGAAGGTCTCCATTTGATATTGTTGGGA
GCTCCGATAACCCTGACCAGAACACAGAGGATTATCTCTTCCAAGTTATTTTGGAAAAACAAATTCGCAT
ACCACGTTCTATGTCTGTAAAAGCTGCAAGTGTTCTGAAGAGTTTTCTTAATAAGGACCCTAAGGAACGA
TTGGGTTGTCTTCCTCAAACAGGATTTGCTGATATTCAGGGACACCCGTTCTTCCGAAATGTTGATTGGG
ATATGATGGAGCAAAAACAGGTGGTACCTCCCTTTAAACCAAATATTTCTGGGGAATTTGGTTTGGACAA
CTTTGATTCTCAGTTTACTAATGAACGTGTCCAGCTCACTCCAGATGACGATGACATTGTGAGGAAGATT
GATCAGTCTGAATTTGAAGGTTTTGAGTATATCAATCCTCTTTTGATGTCTGCAGAAGAATGTGTCTGAT
CCTCATTTTTCAACCATGTATTCTACTCATGTTGCCATTTAATGCATGGATAAACTTGCTGCAAGCCTGG
ATACAATTAACCATTTTATATTTGCCACCTACAAAAAAACACCCAATATCTTCTCTTGTAGACTATATGA
ATCAATTATTACATCTGTTTTACTATGAAAAAAAAATTAATACTACTAGCTTCCAGACAATCATGTCAAA
ATTTAGTTGAACTGGTTTTTCAGTTTTTAAAAGGCCTACAGATGAGTAATGAAGTTATCTTTTTTGTTTA
AAAAAAAAAAAAAA

>gi|10864649|ref|NM_002744.2| Homo sapiens protein kinase C, zeta (PRKCZ), mRNA
ATGCCCAGCAGGACCGACCCCAAGATGGAAGGGAGCGGCGGCCGCGTCCGCCTCAAGGCGCATTACGGGG
GGGACATCTTCATCACCAGCGTGGACGCCGCCACGACCTTCGAGGAGCTCTGTGAGGAAGTGAGAGACAT
GTGTCGTCTGCACCAGCAGCACCCGCTCACCCTCAAGTGGGTGGACAGCGAAGGTGACCCTTGCACGGTG
TCCTCCCAGATGGAGCTGGAAGAGGCTTTCCGCCTGGCCCGTCAGTGCAGGGATGAAGGCCTCATCATTC
ATGTTTTCCCGAGCACCCCTGAGCAGCCTGGCCTGCCATGTCCGGGAGAAGACAAATCTATCTACCGCCG
GGGAGCCAGAAGATGGAGGAAGCTGTACCGTGCCAACGGCCACCTCTTCCAAGCCAAGCGCTTTAACAGG
AGAGCGTACTGCGGTCAGTGCAGCGAGAGGATATGGGGCCTCGCGAGGCAAGGCTACAGGTGCATCAACT
GCAAACTGCTGGTCCATAAGCGCTGCCACGGCCTCGTCCCGCTGACCTGCAGGAAGCATATGGATTCTGT
CATGCCTTCCCAAGAGCCTCCAGTAGACGACAAGAACGAGGACGCCGACCTTCCTTCCGAGGAGACAGAT
GGAATTGCTTACATTTCCTCATCCCGGAAGCATGACAGCATTAAAGACGACTCGGAGGACCTTAAGCCAG
TTATCGATGGGATGGATGGAATCAAAATCTCTCAGGGGCTTGGGCTGCAGGACTTTGACCTAATCAGAGT
CATCGGGCGCGGGAGCTACGCCAAGGTTCTCCTGGTGCGGTTGAAGAAGAATGACCAAATTTACGCCATG
AAAGTGGTGAAGAAAGAGCTGGTGCATGATGACGAGGATATTGACTGGGTACAGACAGAGAAGCACGTGT
TTGAGCAGGCATCCAGCAACCCCTTCCTGGTCGGATTACACTCCTGCTTCCAGACGACAAGTCGGTTGTT
CCTGGTCATTGAGTACGTCAACGGCGGGGACCTGATGTTCCACATGCAGAGGCAGAGGAAGCTCCCTGAG
GAGCACGCCAGGTTCTACGCGGCCGAGATCTGCATCGCCCTCAACTTCCTGCACGAGAGGGGGATCATCT
ACAGGGACCTGAAGCTGGACAACGTCCTCCTGGATGCGGACGGGCACATCAAGCTCACAGACTACGGCAT

GTGCAAGGAAGGCCTGGGCCCTGGTGACACAACGAGCACTTTCTGCGGAACCCCGAATTACATCGCCCCC
GAAATCCTGCGGGGAGAGGAGTACGGGTTCAGCGTGGACTGGTGGGCGCTGGGAGTCCTCATGTTTGAGA
TGATGGCCGGGCGCTCCCCGTTCGACATCATCACCGACAACCCGGACATGAACACAGAGGACTACCTTTT
CCAAGTGATCCTGGAGAAGCCCATCCGGATCCCCCGGTTCCTGTCCGTCAAAGCCTCCCATGTTTTAAAA
GGATTTTTAAATAAGGACCCCAAAGAGAGGCTCGGCTGCCGGCCACAGACTGGATTTTCTGACATCAAGT
CCCACGCGTTCTTCCGCAGCATAGACTGGGACTTGCTGGAGAAGAAGCAGGCGCTCCCTCCATTCCAGCC
ACAGATCACAGACGACTACGGTCTGGACAACTTTGACACACAGTTCACCAGCGAGCCCGTGCAGCTGACC
CCAGACGATGAGGATGCCATAAAGAGGATCGACCAGTCAGAGTTCGAAGGCTTTGAGTATATCAACCCAT
TATTGCTGTCCACCGAGGAGTCGGTGTGAGGCCGCGTGCGTCTCTGTCGTGGACACGCGTGATTGACCCT
TTAACTGTATCCTTAACCACCGCATATGCATGCCAGGCTGGGCACGGCTCCGAGGGCGGCCAGGGACAGA
CGCTTGCGCCGAGACCGCAGAGGGAAGCGTCAGCGGGCGCTGCTGGGAGCAGAACAGTCCCTCACACCTG
GCCCGGCAGGCAGCTTCGTGCTGGAGGAACTTGCTGCTGTGCCTGCGTCGCGGCGGATCCGCGGGGACCC
TGCCGAGGGGGCTGTCATGCGGTTTCCAAGGTGCACATTTTCCACGGAAACAGAACTCGATGCACTGACC
TGCTCCGCCAGGAAAGTGAGCGTGTAGCGTCCTGAGGAATAAAATGTTCCGATGAAAAAAAAAA

>gi|4759123|ref|NM_004171.1| Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 2 (SLC1A2), nuclear gene encoding mitochondrial protein, mRNA
GATAGTGCTGAAGAGGAGGGGCGTTCCCAGACCATGGCATCTACGGAAGGTGCCAACAATATGCCCAAGC
AGGTGGAAGTGCGAATGCCAGACAGTCATCTTGGCTCAGAGGAACCCAAGCACCGGCACCTGGGCCTGCG
CCTGTGTGACAAGCTGGGGAAGAATCTGCTGCTCACCCTGACGGTGTTTGGTGTCATCCTGGGAGCAGTG
TGTGGAGGGCTTCTTCGCTTGGCATCTCCCATCCACCCTGATGTGGTTATGTTAATAGCCTTCCCAGGGG
ATATACTCATGAGGATGCTAAAAATGCTCATTCTCCCTCTAATCATCTCCAGCTTAATCACAGGGTTGTC
AGGCCTGGATGCTAAGGCTAGTGGCCGCTTGGGCACGAGAGCCATGGTGTATTACATGTCCACGACCATC
ATTGCTGCAGTACTGGGGGTCATTCTGGTCTTGGCTATCCATCCAGGCAATCCCAAGCTCAAGAAGCAGC
TGGGGCCTGGGAAGAAGAATGATGAAGTGTCCAGCCTGGATGCCTTCCTGGACCTTATTCGAAATCTCTT
CCCTGAAAACCTTGTCCAAGCCTGCTTTCAACAGATTCAAACAGTGACGAAGAAAGTCCTGGTTGCACCA
CCGCCAGACGAGGAGGCCAACGCAACCAGCGCTGAAGTCTCTCTGTTGAACGAGACTGTGACTGAGGTGC
CGGAGGAGACTAAGATGGTTATCAAGAAGGGCCTGGAGTTCAAGGATGGGATGAACGTCTTAGGTCTGAT
AGGGTTTTTCATTGCTTTTGGCATCGCTATGGGGAAGATGGGAGATCAGGCCAAGCTGATGGTGGATTTC
TTCAACATTTTGAATGAGATTGTAATGAAGTTAGTGATCATGATCATGTGGTACTCTCCCCTGGGTATCG
CCTGCCTGATCTGTGGAAAGATCATTGCAATCAAGGACTTAGAAGTGGTTGCTAGGCAACTGGGGATGTA
CATGGTAACAGTGATCATAGGCCTCATCATCCACGGGGGCATCTTTCTCCCCTTGATTTACTTTGTAGTG
ACCAGGAAAAACCCCTTCTCCCTTTTTGCTGGCATTTTCCAAGCTTGGATCACTGCCCTGGGCACCGCTT
CCAGTGCTGGAACTTTGCCTGTCACCTTTCGTTGCCTGGAAGAAAATCTGGGGATTGATAAGCGTGTGAC
TAGATTCGTCCTTCCTGTTGGAGCAACCATTAACATGGATGGTACAGCCCTTTATGAAGCGGTGGCCGCC
ATCTTTATAGCCCAAATGAATGGTGTTGTCCTGGATGGAGGACAGATTGTGACTGTAAGCCTCACAGCCA
CCCTGGCAAGCGTCGGCGCGGCCAGTATCCCCAGTGCCGGGCTGGTCACCATGCTCCTCATTCTGACAGC
CGTGGGCCTGCCAACAGAGGACATCAGCTTGCTGGTGGCTGTGGACTGGCTGCTGGACAGGATGAGAACT
TCAGTCAATGTTGTGGGTGACTCTTTTGGGGCTGGGATAGTCTATCACCTCTCCAAGTCTGAGCTGGATA
CCATTGACTCCCAGCATCGAGTGCATGAAGATATTGAAATGACCAAGACTCAATCCATTTATGATGACAT
GAAGAACCACAGGGAAAGCAACTCTAATCAATGTGTCTATGCTGCACACAACTCTGTCATAGTAGATGAA
TGCAAGGTAACTCTGGCAGCCAATGGAAAGTCAGCCGACTGCAGTGTTGAGGAAGAACCTTGGAAACGTG
AGAAATAAGGATATGAGTCTCAGCAAATTCTTGAATAAACTCCCCAGCGT

>gi|31543627|ref|NM_004172.2| Homo sapiens solute carrier family 1 (glial high affinity glutamate transporter), member 3 (SLC1A3), mRNA
AGCGGGGTAGTAACTTGCAGTTTCAGAGCACATGCACACTGTCAGGGCTAGCCTGCCTGCTTACGCGCGC
TGCGGATTGTTGCTCCGTTGTACCTGCTGGGGAATTCACCTCGTTACTGCTCGATATCTTCCACCCCTTA
CAAAATCAGAAAAGTTGTGTTTTCTAATACCAAAGAGGAGGTTTGGCTTTCTGTGGGTGATTCCCAGACA
CTGAAGTGCAAAGAAGAGACCCTCCTAGAAAAGTAAAATATGACTAAAAGCAATGGAGAAGAGCCCAAGA
TGGGGGGCAGGATGGAGAGATTCCAGCAGGGAGTCAGTAAACGCACACTTTTGGCCAAGAAGAAAGTGCA
GAACATTACAAAGGAGGATGTTAAAAGTTACCTGTTTCGGAATGCTTTTGTGCTGCTCACAGTCACCGCT
GTCATTGTGGGTACAATCCTTGGATTTACCCTCCGACCATACAGAATGAGCTACCGGGAAGTCAAGTACT
TCTCCTTTCCTGGGGAACTTCTGATGAGGATGTTACAGATGCTGGTCTTACCACTTATCATCTCCAGTCT
TGTCACAGGAATGGCGGCGCTAGATAGTAAGGCATCAGGGAAGATGGGAATGCGAGCTGTAGTCTATTAT
ATGACTACCACCATCATTGCTGTGGTGATTGGCATAATCATTGTCATCATCATCCATCCTGGGAAGGGCA

CAAAGGAAAACATGCACAGAGAAGGCAAAATTGTACGAGTGACAGCTGCAGATGCCTTCCTGGACTTGAT
CAGGAACATGTTCCCTCCAAATCTGGTAGAAGCCTGCTTTAAACAGTTTAAAACCAACTATGAGAAGAGA
AGCTTTAAAGTGCCCATCCAGGCCAACGAAACGCTTGTGGGTGCTGTGATAAACAATGTGTCTGAGGCCA
TGGAGACTCTTACCCGAATCACAGAGGAGCTGGTCCCAGTTCCAGGATCTGTGAATGGAGTCAATGCCCT
GGGTCTAGTTGTCTTCTCCATGTGCTTCGGTTTTGTGATTGGAAACATGAAGGAACAGGGGCAGGCCCTG
AGAGAGTTCTTTGATTCTCTTAACGAAGCCATCATGAGACTGGTAGCAGTAATAATGTGGTATGCCCCCG
TGGGTATTCTCTTCCTGATTGCTGGGAAGATTGTGGAGATGGAAGACATGGGTGTGATTGGGGGGCAGCT
TGCCATGTACACCGTGACTGTCATTGTTGGCTTACTCATTCACGCAGTCATCGTCTTGCCACTCCTCTAC
TTCTTGGTAACACGGAAAAACCCTTGGGTTTTTATTGGAGGGTTGCTGCAAGCACTCATCACCGCTCTGG
GGACCTCTTCAAGTTCTGCCACCCTACCCATCACCTTCAAGTGCCTGGAAGAGAACAATGGCGTGGACAA
GCGCGTCACCAGATTCGTGCTCCCCGTAGGAGCCACCATTAACATGGATGGGACTGCCCTCTATGAGGCT
TTGGCTGCCATTTTCATTGCTCAAGTTAACAACTTTGAACTGAACTTCGGACAAATTATTACAATCAGCA
TCACAGCCACAGCTGCCAGTATTGGGGCAGCTGGAATTCCTCAGGCGGGCCTGGTCACTATGGTCATTGT
GCTGACATCTGTCGGCCTGCCCACTGACGACATCACGCTCATCATCGCGGTGGACTGGTTCCTGGATCGC
CTCCGGACCACCACAAACGTACTGGGAGACTCCCTGGGAGCTGGGATTGTGGAGCACTTGTCACGACATG
AACTGAAGAACAGAGATGTTGAAATGGGTAACTCAGTGATTGAAGAGAATGAAATGAAGAAACCATATCA
ACTGATTGCACAGGACAATGAAACTGAGAAACCCATCGACAGTGAAACCAAGATGTAGACTAACATAAAG
AAACACTTTCTTGAGCACCAGGTGTTAAAAACCATTATAAAATCTTTCCATCTCATTACAGCTCATTCGC
TCCAGCAAGCCCGTCATCTTCCCTTTCCTCCCTTCTGATAAGACTGGAAAATAGTCCTCCAAAACACAAG
GGAGGATTTTGGGTGGCCAAAGTGTACAATTTTCATCCCACAATTGAAATTTTTAAATCATTTCATGTTA
GTCTTACCGAATAAGGTACCAAGATCACAAATAGTGTTGATCAGATCTTACAAGTTTATGTGGCACACAA
TCCTATAAATGTGATTTTTTTATATAAGTTAAAGAGACAAATAGTAGGCTAAAAACATTTTAAAATCAAC
TTTTGAAATTTAAAAATCTTTCAGAATACAATTCAGTTTTAGTTTCAAAATGTTAACAACTTGAATTACA
ACCGGTTATCAGTTGGACAGTAAGATTTTATCCCTTTCTCTTCTGACTGGTATACCTATTTCATTAGTAG
CTAGGTGCACATATACATCTAGCACAGCTGTGAGGACAGACAGAAGGCAAAGTTTCCATGTGGCCTTGAG
CAAGTCCCATCTCACCTCTAGGCCTCAGTGTCCTCATCTATAAAATGAGGGACTTCCCTAGAAGTCTTCA
TGGTCTCTTCCAGCCCAGACATCCTGTGATGTCATGAAAGCACCTGCCCTCTGTTTCCCCTCAGAACACC
CTGTACCATCCATGGAGCACGAGGCCTTCAGAAAAGACACTTCAATGGGAGTGAACATTTCTAACTAAGG
ACAGGATGGCTGTGTGTGGTGGTCACCAGGTCCTGTGAGCAAAGTGCAGGTTATGCAAGTCGCCAGGCAG
GAGGCCATTCCAGGAGTGGGATTATTCATCAAACTCTTTGCCCAGTTCATCCCAATGGGGGAAGTATTCC
CTTCTTTCCTACTCTGGGAAGAATGTCTCCTGCCACTCCTCAACTGATGATAGACTTCGAAAACAGATGA
GAAGACTAGCAGCTAGCAAGGGTGCTTGTAGTCACACTGTGGAACACTAAAGAGCTAGGAAAGAGTTGAG
CACAGGCAACATTACAAACAAAGGATTTGAAAACACCAAGAGTACAGGTCTTCTTTAAGGAAGAATAAAA
AAGAAGAGGTTCATTTTTCTGGCTTTTTTTTTCACCTGAAACACTTTTTCTCGAGTCCAAAATCATTCCC
CCCGTGAAGTCTGCTTACCAAAACATAAGACGACTTATATATTTGAAAGAAGTCAAATGAATGAGCTCTC
TAATAGAAGTCCATGAGTTGAGTGGGTATTTCTTATTTGAAAGTGTTTTTCTTTAATCAAAAGTCCTTAG
AATGAGGGAAACAAAATATTTATTTGTTTTGGAATCCCACTTATCAAATCATTCAAAACTTTCAGCTGGA
GTGGGGTTTGCTTTTGTTTTGTTTGTGTCCATAAGAGAAATGGTAGAAGATGAATCAGTATGAAGACACT
GTCAATGAGGTTATGAGAAAAACAGCAGGGGCATTAGTTTCAGGCAAGGCAGCTCCCAGGTTTAGAGATT
AATTTTTACCCCCTAAGGAATATCCAGTCAAAGACGCTGAGTGGGAGCTGTCAGGCAGTAGCAGCTGTGT
TTGAGTTTCTGGCTGAAAATGGTGAAGAATGGACTTAATCATGCTAACAAACTGAAAAATCTAGACATAG
ATCCTCTGATATACAATTAGAGATATTTTTATATAGACCCCAAGCATTCTGTGCATAAAAGTTAACATTA
GGCTGTGGTGCAGTAACCATTTAATGTCGAGGCTCTATTTCGGAAATACACTACAAATGTTAAAGTACGT
GGCTGTCCTCTTAAGACACTAGTAGAGCAAAGACTTAATCATATCAACTTAATTCTGTTACACAATATGT
GTTTTTTTAATATACTAACCATTTCTTATGGAAAGGTCCTGTGGGGAGCCCATCATCTCGCCAAGCCATC
ACAGGCTCTGCATACACATGCACTCAGTGTGGACTGGGAAGCATTACTTTGTAGATGTATTTTCAATAAA
GAAAAAAATAGTTTTACATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAA

>gi|20070238|ref|NM_006671.2| Homo sapiens solute carrier family 1 (glutamate transporter), member 7 (SLC1A7), mRNA
GGCACGAGGCTGGTGTTTAGCAACTCCGACCACCTGCCTGCTGAGGGGCTAGAGCCCTCAGCCCAGACCC
TGTGCCCCCGGCCGGGCTCTCATGCGTGGAATGGTGCTGTGCCCCTTGCCAGCAGGCCAGGCTCACCATG
GTGCCGCATGCCATCTTGGCACGGGGGAGGGACGTGTGCAGGCGGAATGGACTCCTCATCCTGTCTGTGC
TGTCTGTCATCGTGGGCTGCCTCCTCGGCTTCTTCTTGAGGACCCGGCGCCTCTCACCACAGGAAATTAG
TTACTTCCAGTTCCCTGGAGAGCTCCTGATGAGGATGCTGAAGATGATGATCCTGCCACTGGTGGTCTCC
AGCTTGATGTCCGGACTTGCCTCCCTGGATGCCAAGACCTCTAGCCGCCTGGGCGTCCTCACCGTGGCGT
ACTACCTGTGGACCACCTTCATGGCTGTCATCGTGGGCATCTTCATGGTCTCCATCATCCACCCAGGCAG

CGCGGCCCAGAAGGAGACCACGGAGCAGAGTGGGAAGCCCATCATGAGCTCAGCCGATGCCCTGTTGGAC
CTCATCCGGAACATGTTCCCAGCCAACCTAGTAGAAGCCACATTCAAACAGTACCGCACCAAGACCACCC
CAGTTGTCAAGTCCCCCAAGGTGGCACCAGAGGAGGCCCCTCCTCGGCGGATCCTCATCTACGGGGTCCA
GGAGGAGAATGGCTCCCATGTGCAGAACTTCGCCCTGGACCTGACCCCGCCGCCCGAGGTCGTTTACAAG
TCAGAGCCGGGCACCAGCGATGGCATGAATGTGCTGGGCATCGTCTTCTTCTCTGCCACCATGGGCATCA
TGCTGGGCCGCATGGGTGACAGCGGGGCCCCCCTGGTCAGCTTCTGCCAGTGCCTCAATGAGTCGGTCAT
GAAGATCGTGGCGGTGGCTGTGTGGTATTTCCCCTTCGGCATTGTGTTCCTCATTGCGGGTAAGATCCTG
GAGATGGACGACCCCAGGGCCGTCGGCAAGAAGCTGGGCTTCTACTCAGTCACCGTGGTGTGCGGGCTGG
TGCTCCACGGGCTCTTTATCCTGCCCCTGCTCTACTTCTTCATCACCAAGAAGAATCCCATCGTCTTCAT
CCGCGGCATCCTGCAGGCTCTGCTCATCGCGCTGGCCACCTCCTCCAGCTCAGCCACACTGCCCATCACC
TTCAAGTGCCTGCTGGAGAACAACCACATCGACCGGCGCATCGCTCGCTTCGTGCTGCCCGTGGGTGCCA
CCATCAACATGGACGGCACTGCGCTCTACGAGGCTGTGGCCGCCATCTTCATCGCCCAGGTCAACAACTA
CGAGCTGGACTTTGGCCAGATCATCACCATCAGTATCACAGCCACTGCAGCCAGCATTGGGGCAGCTGGC
ATCCCCCAGGCCGGCCTCGTCACCATGGTCATCGTGCTCACCTCCGTGGGACTGCCCACCGATGACATCA
CCCTCATCATTGCCGTTGACTGGGCTCTGGACCGTTTCCGCACCATGATTAACGTGCTGGGTGATGCGCT
GGCAGCGGGGATCATGGCCCATATATGTCGGAAGGATTTTGCCCGGGACACAGGCACCGAGAAACTGCTG
CCCTGCGAGACCAAGCCAGTGAGCCTCCAGGAGATCGTGGCAGCCCAGCAGAATGGCTGTGTGAAGAGTG
TAGCCGAGGCCTCCGAGCTCACCCTGGGCCCCACCTGCCCCCACCACGTCCCCGTTCAAGTGGAGCGGGA
TGAGGAGCTGCCCGCTGCGAGTCTGAACCACTGCACCATCCAGATCAGCGAGCTGGAGACCAATGTCTGA
GCCTGCGGAGCTGCAGGGGCAGGCGAGGCCTCCAGGGGCAGGGTCCTGAGGCAGGAACTCGACTCTCCAA
CCCTCCTGAGCAGCCGGCAGGGGCCAGGATCACACATTCTTCTCACCCTTGAGAGGCTGGAATTAACCCC
GCTTGACGGAAAATGTATCTCAGAGAAGGGAAAGGCTGCATGGGGGAGCCCCATCCAGGGAGTGATGGGC
CCGGCATTGCCTGAGGCCCCGCTGTGACAGTTTCCCCGGTGTGAGCCCGGTGAGGGCGGCAGGCAGGGGT
TATCCGGCCCCACTTTCTGGATGACAGACTTGAGGCTCTGAGAGCTGAAAACACTTGTCCAAGGTCTCAC
GTTAAGGTCAAGACACTAACTCAAATCTTTCAAGCCCCGCCTCTCCTCTTGGAGGACAGGGCAGCCTGCA
GCTGTGTCCAGGCCCAGGCCCCACCCCATAACAGGTGGCCTCAGCCACACAGTTCTCCCCAAGGGGAGCA
GCCCAGGGCCAAGCCCCGCTGCCTTCCCCAGGCCACAGTGCGTCCAGTCTCCTGTCCTGCCACGTGTCTT
TTGCAAAGCTCCTTGGATGTGGAGACAGATGTCTTTACTAGAGCTGAAAGGCCCCCTTGACACATCCAGG
CCAACCTCCCATGGAATAGGTAGGCAAGCCAGGACTCCGGGAAGGAGGTGCAGCCAGGATGCTCTGGTGG
AGCTGCCGATGGGGCCCTGGTGTCAGAACTCCCCAAAGGCCTGTGCGTCCAAGTGGAGTCAGGTTTTCTA
TTCCTTTCTGTGTTTGCAAATTCAGTGTTAACTAAATAAAGGTATTTTGTTTTTCAAAAAAAAAAAAAAA
AAA

>gi|21314631|ref|NM_003038.2| Homo sapiens solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4), mRNA
CCCGCACTCTGCGCCTCTCCTCGCCTTTCTCGCACCTGCTCCTGCGCCAGGCCGCGAGACCCCCGGGGCG
GCTTCCCAGAACCTGCGGAGCACAACTGGCCGACCGACCCATTCATTGGGAACCCCGTCTTTTGCCAGAG
CCCACGTCCCCTGCCACCTCTAGCTCGGAGCGGCGTGTAGCGCCATGGAGAAGAGCAACGAGACCAACGG
CTACCTTGACAGCGCTCAGGCGGGGCCTGCGGCCGGGCCCGGAGCTCCGGGGACCGCGGCGGGACGCGCA
CGGCGTTGCGCGGGCTTCCTGCGGCGCCAAGCGCTGGTGCTGCTCACCGTGTCCGGGGTGCTGGCGGGCG
CGGGCCTGGGCGCGGCGTTGCGCGGGCTCAGCCTGAGCCGCACGCAGGTCACCTACCTGGCCTTCCCCGG
CGAGATGCTGCTCCGCATGCTGCGCATGATCATCCTGCCGCTGGTGGTCTGCAGCCTGGTGTCGGGCGCC
GCCTCCCTCGATGCCAGCTGCCTCGGGCGTCTGGGCGGCATCGCTGTCGCCTACTTTGGCCTCACCACAC
TGAGTGCCTCGGCGCTCGCCGTGGCCTTGGCGTTCATCATCAAGCCAGGATCCGGTGCGCAGACCCTTCA
GTCCAGCGACCTGGGGCTGGAGGACTCGGGGCCTCCTCCTGTCCCCAAAGAGACGGTGGACTCTTTCCTC
GACCTGGCCAGAAACCTGTTTCCCTCCAATCTTGTGGTTGCAGCTTTCCGTACGTATGCAACCGATTATA
AAGTCGTGACCCAGAACAGCAGCTCTGGAAATGTAACCCATGAAAAGATCCCCATAGGCACTGAGATAGA
AGGGATGAACATTTTAGGATTGGTCCTGTTTGCTCTGGTGTTAGGAGTGGCCTTAAAGAAACTAGGCTCC
GAAGGAGAAGACCTCATCCGTTTCTTCAATTCCCTCAACGAGGCGACGATGGTGCTGGTGTCCTGGATTA
TGTGGTACGTACCTGTGGGCATCATGTTCCTTGTTGGAAGCAAGATCGTGGAAATGAAAGACATCATCGT
GCTGGTGACCAGCCTGGGGAAATACATCTTCGCATCTATATTGGGCCATGTTATTCATGGAGGAATTGTT
CTGCCACTTATTTATTTTGTTTTCACACGAAAAAACCCATTCAGATTCCTCCTGGGCCTCCTCGCCCCAT
TTGCGACAGCATTTGCTACCTGCTCCAGCTCAGCGACCCTTCCCTCTATGATGAAGTGCATTGAAGAGAA
CAATGGTGTGGACAAGAGGATCAGCAGGTTTATTCTCCCCATCGGGGCCACCGTGAACATGGACGGAGCA
GCCATCTTCCAGTGTGTGGCCGCGGTGTTCATTGCGCAACTCAACAACGTAGAGCTCAACGCAGGACAGA
TTTTCACCATTCTAGTGACTGCCACAGCGTCCAGTGTTGGAGCAGCAGGCGTGCCAGCTGGAGGGGTCCT
CACCATTGCCATTATCCTGGAGGCCATTGGGCTGCCTACTCATGACCTGCCTCTGATCCTGGCTGTGGAC

TGGATTGTGGACCGGACCACCACGGTGGTGAATGTGGAAGGGGATGCCCTGGGTGCAGGCATTCTCCACC
ACCTGAATCAGAAGGCAACAAAGAAAGGCGAGCAGGAACTTGCTGAGGTGAAAGTGGAAGCCATCCCCAA
CTGCAAGTCTGAGGAGGAGACATCGCCCCTGGTGACACACCAGAACCCCGCTGGCCCCGTGGCCAGTGCC
CCAGAACTGGAATCCAAGGAGTCGGTTCTGTGATGGGGCTGGGCTTTGGGCTTGCCTGCCAGCAGTGATG
TCCCACCCTGTTCACCCAGCCGCCAGTCATGGACACAGGGCACTGCCCTTGCCAACTTTTACCCTCCCAA
GCAATGCTTTGGCCCAGTCGCTGGCCTGAGGCTTACCTCTCGGCACTGGCATTGGGCTCCCCAGCCGGAA
CTGGTTACCAAGGACAAGGACACTCTGACATTCGGCTTGATCCATGTCCAGGTGCAACTGTGTGTACACC
AGGGATCTGTTTGGAAACAACCCCTTGAGCTGCCAGGCTCAAGAAATCATGGACTCACAGGGTCCTGTGT
GGTTACATCTTGGAAAAAATGCAGATGTATTTCACTCTCCCCGGTCAGCTCTGCATCAGGTGTTTTCTGA
GCAAACCAAGGGGGTTTATAGTCATCTGTCGCATTGCCTCGAGTTGCAGTAATTGAAAAAATGCTCAAAT
TCTTAGCCATGGCTGGCCTTTGCTGAGCTGGGACTCAGGTGTTTAAAGAGTTTGTGCTATAGCTAGGTGT
GGATAGCTTCTGATCCCTGGGTTCTGGGAGACTGCAGGTGCCGCACATTGTCAAGTTAGAAATACTCCAG
GTGGGTGTTAGCACTGTGGTGGTCTCTGGTCCACAGCCTTAGGTAAACAACTTAGATTCTGAGGTCAAAG
AAAAAAGGAGAGGGAATGCAGCCTTGTGGGGGAGAAGCGGGGCAGAGGGTTCTCTAATCTAATCAGGACA
GGACAGGTTTCACATACAATTGTCCCAGTTCGCATCCCAGCCCTGGGGCACTTTTCTGCTTCCTTCCAGA
GGCCTGGGCCTCTGATAACACTTTGGCTTTTTCTCCATTCACGCTGATTTGGCAAAAGGCCAGAGATGGG
CCTCCTTCCCTGGGGAGGTGTGATGTAGTTATCACATTCAGGACCCTTGTTGATTTATCATCTATTATTT
GAATTCAACTGGACACTCTGTAAAATGCTGCACTGCAGCAAAAACAAAACCACCACCACCCCAGAGAAAA
CCATGTACTAATTGGAGTGGGGTACCCCCATTCACAGGTTCCCAGGTCCCCTGGCTTTGGCTGATTTCAA
AATATAGAGCCCTTTCTTGCCAGTACATCCAAGTTTAAAATTATCAGCGAAATGGTCCATGTTTTTCCAA
TTACCTGCTGACACGGTTCTAAGCTAAGTGAAGGGGAAGATCTGAGAGCGTGCTGTTTGTGGCTGTTGAT
GCATATTCGTGATGTAACAGGTCCTGGGGCCTCACTTTACCCCATTTGTAAAATGGGGCTAATGTCACCT
GCCTCTTACCTACCTCAGAGGGATTTGGTGAAGCAAACTGTTAATCTTCGAAAACGACCATTTCACTTCT
TGGATATCAAGTGCTAACCCAGTATGTTCTTCTTTTTTATGTAAGGGACAGCTTTGGAGAAAGGACTGCT
CTGTGGAGCAGAGTCCTTTCTGCTGGTGAGGACAGCATTTCTGAGCAGGGCTTTGTTCTCTATGTGCATT
AGGACTTTTATCATGCCCTTGTTCTGTGTGTAGTTACTTGACAGCATCAAATGCCGCCTCTTCCTAATGT
CCTTCAAGTTTTCATGAACTAGCAACCCCACCTTCCACCATGGTTCTGGGCGCCTGATTTTGCTGTGACT
CCCAGACCCAGCCACTGTTTCTGCCACCCTGTAACAGGCCATTAAAGCTCCCCAGTGTTCAGCCTCCTTC
ACTCCCTTGTTTTCCCTGTTGCTATGTGTCACCTGGGCCCTACAGACAGGGGCACACGCTTATGGATGTG
TGTACCATTGAGATGAGAATGGGTAGATGGAACGGAGACCATCAAGCCACACCCCCTTCTTAAAACTGGG
GACATGAGCCTGAGCAGAAAGGGTGAAGAAGAGCCATGGGACACAGAGTTGACCCAGCCAGGGGGAAAGC
CCAGCTCTCTTTAAACCAGCTAAGCCATTCCAGTCTCCTGTGAAGCCAAAAGGGACCAGGAACCGTGCAA
AGGAAACTGGAAACTTTTCCCCGCTGGGTAGAGCATGTTGCTGATACTCTTCTGTTTTCAAGGGAAACAA
TCACATTGTTTGATTCCAAATGGTAAATGAACACTCACTATTCTTCAGGCTTCAGTAAATCTTTTTTTCT
TCCTTCATATATATATACACAACACACACACACATATGTATATCTATACACACATGTGTGTTGTGTATAT
GCATGTGTGTGTGTGTGCGTGTGTGTATAGTTTTAGCTCCAAGCCAAGCAAGTTTGTGTTTGGATAGAGG
GGAACTTAACTATTAACTACAAGTTGTATGTCTGTGGTATCTTGATTTTCCCATTTCTAAAGATGAATTT
CACAAAGCCATAAAGCGTGAAATTAGAGCTGGACTTAAGACTCATTGGCCGACCATCCTGTGTCCTGGCC
TGGCCCTGCAGTAAGAAGCGTGTCTGGGTCTGGAGAAGGGTGCTTCCGAGAGTGTGCAGGTGGCCCTTCC
CCTTGGAGGCGAGAAGAGAGAATGTGCTGTCTATCTTCCTGGTTTTCAGTCCACAGAGTCGGTAGACCAG
GGGTTACGTGACTGGGGAAAATCTCACATCTCCTTGTCTGAAAACATTTCCCCTGCTGTTCTCTTTCTAA
CATGTTGTGGTAAATCTGTTCAGATACTGCTCATCTGACTGTTTTGTACATGTGACAATTGCCTTAAAAC
CTAGCACAGTCCTCAGAAATGAATACCGTGTTTCCACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

>gi|4827011|ref|NM_005071.1| Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
GATAGACCATGAGCAGCCATGGCAACAGCCTGTTCCTTCGGGAGAGCGGCCAGCGGCTGGGCCGGGTGGG
CTGGCTGCAGCGGCTGCAGGAAAGCCTGCAGCAGAGAGCACTGCGCACGCGCCTGCGCCTGCAGACCATG
ACCCTCGAGCACGTGCTGCGCTTCCTGCGCCGAAACGCCTTCATTCTGCTGACGGTCAGCGCCGTGGTCA
TTGGGGTCAGCCTGGCCTTTGCCCTGCGCCCATATCAGCTCACCTACCGCCAGATCAAGTACTTCTCTTT
TCCTGGAGAGCTTCTGATGAGGATGCTGCAGATGCTGGTGTTACCTCTCATTGTCTCCAGCCTGGTCACA
GGTATGGCATCCCTGGACAACAAGGCCACGGGGCGGATGGGGATGCGGGCAGCTGTGTACTACATGGTGA
CCACCATCATCGCGGTCTTCATCGGCATCCTCATGGTCACCATCATCCATCCCGGGAAGGGCTCCAAGGA
GGGGCTGCACCGGGAGGGCCGGATCGAGACCATCCCCACAGCTGATGCCTTCATGGACCTGATCAGAAAT
ATGTTTCCACCAAACCTTGTGGAGGCCTGCTTCAAACAGTTCAAGACGCAGTACAGCACGAGGGTGGTAA
CCAGGACCATGGTGAGGACAGAGAACGGGTCTGAGCCGGGTGCCTCCATGCCTCCTCCATTCTCAGTGGA

GAACGGAACCAGCTTCCTGGAAAATGTCACTCGGGCCTTGGGTACCCTGCAGGAGATGCTGAGCTTTGAG
GAGACTGTACCCGTGCCTGGCTCCGCCAATGGCATCAACGCCCTGGGCCTCGTGGTCTTCTCTGTGGCCT
TTGGGCTGGTCATTGGTGGCATGAAACACAAGGGCAGAGTCCTCAGGGACTTCTTCGACAGCCTCAATGA
GGCTATTATGAGGCTGGTGGGCATCATTATCTGGTATGCACCTGTGGGCATCCTGTTCCTGATTGCTGGG
AAGATTCTGGAGATGGAAGACATGGCCGTCCTGGGGGGTCAGCTGGGCATGTACACCCTGACCGTCATCG
TGGGCCTGTTCCTCCATGCCGGCATTGTCCTTCCCCTCATCTACTTCCTCGTCACTCACCGGAACCCCTT
CCCCTTCATTGGGGGCATGCTACAAGCCCTCATCACCGCTATGGGCACGTCTTCCAGCTCGGCAACGCTG
CCCATCACCTTCCGCTGCCTGGAGGAGGGCCTGGGTGTGGACCGCCGCATCACCAGGTTCGTCCTGCCCG
TGGGCGCCACGGTCAACATGGATGGCACTGCCCTCTACGAGGCCCTGGCTGCCATCTTCATTGCTCAAGT
TAACAACTACGAGCTCAACCTGGGTCAGATCACAACCATCAGCATCACGGCCACAGCAGCCAGTGTTGGG
GCTGCTGGCATCCCCCAGGCGGGTCTGGTCACCATGGTCATTGTGCTTACGTCGGTCGGCTTGCCCACGG
AAGACATCACGCTCATCATCGCCGTGGACTGGTTCCTTGACCGGCTTCGCACAATGACCAACGTACTGGG
GGACTCAATTGGAGCGGCCGTCATCGAGCACTTGTCTCAGCGGGAGCTGGAGCTTCAGGAAGCTGAGCTT
ACCCTCCCCAGCCTGGGGAAACCCTACAAGTCCCTCATGGCACAGGAGAAGGGGGCATCCCGGGGACGGG
GAGGCAACGAGAGTGCTATGTGAGGGGCCTCCAGCTCTG

>gi|31543625|ref|NM_004170.3| Homo sapiens solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 (SLC1A1), mRNA
AGCGGAGGAGCCGGGCGCGCCTGCCACGCAAAACTACCGGGCTGGCAGGGCGGCGGGCGCGGTGCGCGAT
CCCGGGTGGCGGCGGCAACGGCGGTGGTGACGGCGGCGACTGCAGCGGCCGGCTCTCACCTCTCCCCTGT
GCACCCGCATCTCGCCGCGCCGCCGAGCAGCCAGCAGTCCCCGGGTCGCCCAGCCCACGCGCGCACGGCC
GAGCCCAGCGCACAATAGCGGCGACAGCCATGGGGAAACCGGCGAGGAAAGGATGCGAGTGGAAGCGCTT
CCTGAAGAATAACTGGGTGTTGCTGTCCACCGTGGCCGCGGTGGTGCTAGGCATTACCACAGGAGTCTTG
GTTCGAGAACACAGCAACCTCTCAACTCTAGAGAAATTCTACTTTGCTTTTCCTGGAGAAATTCTAATGC
GGATGCTGAAACTCATCATTTTGCCATTAATTATATCCAGCATGATTACAGGTGTTGCTGCACTGGATTC
CAACGTATCCGGAAAAATTGGTGTGCGCGCTGTCGTGTATTATTTCTGTACCACTCTCATTGCTGTTATT
CTAGGTATTGTGCTGGTGGTGAGCATCAAGCCTGGTGTCACCCAGAAAGTGGGTGAAATTGCGAGGACAG
GCAGCACCCCTGAAGTCAGTACGGTGGATGCCATGTTAGATCTCATCAGGAATATGTTCCCTGAGAATCT
TGTCCAGGCCTGTTTTCAGCAGTACAAAACTAAGCGTGAAGAAGTGAAGCCTCCCAGCGATCCAGAGATG
AACATGACAGAAGAGTCCTTCACAGCTGTCATGACAACTGCAATTTCCAAGAACAAAACAAAGGAATACA
AAATTGTTGGCATGTATTCAGATGGCATAAACGTCCTGGGCTTGATTGTCTTTTGCCTTGTCTTTGGACT
TGTCATTGGAAAAATGGGAGAAAAGGGACAAATTCTGGTGGATTTCTTCAATGCTTTGAGTGATGCAACC
ATGAAAATCGTTCAGATCATCATGTGTTATATGCCACTAGGTATTTTGTTCCTGATTGCTGGGAAGATCA
TAGAAGTTGAAGACTGGGAAATATTCCGCAAGCTGGGCCTTTACATGGCCACAGTCCTGACTGGGCTTGC
AATCCACTCCATTGTAATTCTCCCGCTGATATATTTCATAGTCGTACGAAAGAACCCTTTCCGATTTGCC
ATGGGAATGGCCCAGGCTCTCCTGACAGCTCTCATGATCTCTTCCAGTTCAGCAACACTGCCTGTCACCT
TCCGCTGTGCTGAAGAAAATAACCAGGTGGACAAGAGGATCACTCGATTCGTGTTACCCGTTGGTGCAAC
AATCAACATGGATGGGACTGCGCTCTATGAAGCAGTGGCAGCGGTGTTTATTGCACAGTTGAATGACCTG
GACTTGGGCATTGGGCAGATCATCACCATCAGTATCACGGCCACATCTGCCAGCATCGGAGCTGCTGGCG
TGCCCCAGGCTGGCCTGGTGACCATGGTGATTGTGCTGAGTGCCGTGGGCCTGCCCGCCGAGGATGTCAC
CCTGATCATTGCTGTCGACTGGCTCCTGGACCGGTTCAGGACCATGGTCAACGTCCTTGGTGATGCTTTT
GGGACGGGCATTGTGGAAAAGCTCTCCAAGAAGGAGCTGGAGCAGATGGATGTTTCATCTGAAGTCAACA
TTGTGAATCCCTTTGCCTTGGAATCCACAATCCTTGACAACGAAGACTCAGACACCAAGAAGTCTTATGT
CAATGGAGGCTTTGCAGTAGACAAGTCTGACACCATCTCATTCACCCAGACCTCACAGTTCTAGGGCCCC
TGGCTGCAGATGACTGGAAACAAGGAAGGACATTTCCGTGAGAGTCATCTCAAACACTGCTTAAGGAAAA
GAGAAACACTAATGGCCAAGTGTACATTTGATTTGATATACAGACCTCCAGATTATTTTCTATATTTGGA
TTCACAGCCTTTGCGCTCTGGGTTTTGGGATTTGGGTGTGGGGTAAGTTGAAGGGAAATCAATTTAAAGG
AAAGTTCTATTATCTGGGTTTTAGAAATTCTATAAGAGACAAAGTTTGGAAGTACATAAAGTAATAACTG
TTAGAATTAGGTAATGGATATGAAAGAGAAAATGCTTTCTCATGCATAGACAAGTGTTTTGGGTTTTTAA
AAAAAATATTCTGTCATTGGTTACAAATTTTTACTCAGGCTTTCTATTGGCATGGATTTCCTTTGACCTC
TCACTTTTTTATAAATTATAATGCATCTAAACCACCTGTCCCCAGTTAATGTGCCAAAATGTCAATTTTT
AACTTATCTCCAGCCAATTTCAAAGAAAACAGACCAGCATAGTTCTGCAATAACAGTTTTAAGATGGGCA
TAGGGTTTGGAAGAAAGAGAGAAGGATTCTTTTTTCAATGTACTGTATTGGGACGCTGGTAACTGTTAAC
CCAGTGTTCAGCATAGAGCTATATATATATATATATATGTATATATTTATTATTTTCATATAATTTGCCAGA
CAGAGATCAGAATTGAACCGTCAATGTGAAATAAAGAGTTCTCCTTGTACTTGAATAATAACCACGATTC
CAACCCAGGTCTGCTTTGGGGCTTATCAGAACTCCTTTCTAAGGAGCACTAGAATGAGAAATCATGTTGT

TCGATCGTTTCACATCTGTATATCAGCTCTAAAGCAGAGATGTATTATGGTGATACTCCAAGGTGGCATA
GCCATTCATTTACAACTTCCAGATTTGAGCTGCCTGGAGGGAATCCATATCAGCTCTGCATAAGATTATA
TACAAAGCTGTCACTCACAAAAGGCTGGATGTGCTTTCATCCAACTGGAAGGCTTTATTCTTCCAAGTTC
ATTCATACTCAAAGAGGCCAGTACTTTGCCATCCTTGCACTTTCTGTTATCAGGGCCCAAATAACAGTGG
CAAGCTACCAACTAAGTTGTATTTTAATAAAGATTCCATGGGTTGAACAAGCCACGTTGCAGAAAAAGAG
CTTCCCCTAACCTGGGTTGTTGCAGAGTAAATCCCACGACATAAGCTGGTATCACTGGTTCGGGGGAAAT
AGTTCCATTCTATGACTCTTGTCTCCTCCTCCAGGAGGACTGTTCTAACTAGTAATCTTGGCCCTATTCA
TTACATCCTCTGCTTGTCATTCTGCTAATTTATGAAGATAGTTTATTATAGTCTGTACTTCAGTTCTCAT
CTTGTAAATAATGCTTAACATAAACTTGTACTTACACTGAAATCCAAAATAGTCATGTTTCTGCAGTATT
CTGTAGCCAACTTAAACCTGTGCTTTCATGTTTAAGAAATGAGAAATTGTGCCAAAGATAGCAGAAGAGT
AGATAAGTGCTCAGTATTGACGACCTACATCTGAAATCTACAACATAATGATACTGAATTGTTATGTAAA
CATCATAAATAGTAAATAATGATTCAATGTGAATTTTAAAATGCAAATATTGCTATTGTTTATAGGAAAT
AAATCTAAATATAAACGAAAAAAAAAAAAAAAA

>gi|5032092|ref|NM_005628.1| Homo sapiens solute carrier family 1
(neutral amino acid transporter), member 5 (SLC1A5), mRNA
GTAACCGCTACTCCCGGACACCAGACCACCGCCTTCCGTACACAGGGGCCCGCATCCCACCCTCCCGGAC
CTAAGAGCCTGGGTCCCCTGTTTCCGGAGGTCCGCTTCCCGGCCCCCAGATTCTGGCATCCCAGCCCTCA
GTGTCCAAGACCCAGGCAGCCCGGGTCCCCGCCTCCCGGATCCAGGCGTCCGGGATCTGCGCCACCAGAA
CCTAGCCTCCTGCAGACCTCCGCCATCTGGGGGCACTCAACCTCCTGGAGCCAAGGGCCCCACGTCCCAC
CCAGAGAAACTCTCGTATTCCCAGCTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACTCCCAGCTTTCGG
ACATCTGGCACACGGGGCAGAGCAGAGAAGCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCC
AAGAGCCAAGGAACTTCAGTGCTGTGAACTCACAACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGT
GCTGTTACTCAACTCAGTCCTAGGAACGTCGGGTCCTGGGAAGGAGCCCAAGCGCTCCCAGCCAGCTTCC
AGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATCCTCCTCGAGACTCCAAGGGGCTCGCAG
CGGCGGAGCCCACCGCCAACGGGGGCCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGGCGG
CTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTGTGCTGCTGACAGTGGTG
GCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCCGGGGGTGCGCTGGCGTTGGGCCCGG
AGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCTGCTGCTGCGTCTGCTGCGGATGATCATCTTGCCGCT
GGTGGTGTGCAGCTTGATCGGCGGCGCCGCCAGCCTGGACCCCGGCGCGCTCGGCCGTCTGGGCGCCTGG
GCGCTGCTCTTTTTCCTGGTCACCACGCTGCTGGCGTCGGCGCTCGGAGTGGGCTTGGCGCTGGCTCTGC
AGCCGGGCGCCGCCTCCGCCGCCATCAACGCCTCCGTGGGAGCCGCGGGCAGTGCCGAAAATGCCCCCAG
CAAGGAGGTGCTCGATTCGTTCCTGGATCTTGCGAGAAATATCTTCCCTTCCAACCTGGTGTCAGCAGCC
TTTCGCTCATACTCTACCACCTATGAAGAGAGGAATATCACCGGAACCAGGGTGAAGGTGCCCGTGGGGC
AGGAGGTGGAGGGGATGAACATCCTGGGCTTGGTAGTGTTTGCCATCGTCTTTGGTGTGGCGCTGCGGAA
GCTGGGGCCTGAAGGGGAGCTGCTTATCCGCTTCTTCAACTCCTTCAATGAGGCCACCATGGTTCTGGTC
TCCTGGATCATGTGGTACGCCCCTGTGGGCATCATGTTCCTGGTGGCTGGCAAGATCGTGGAGATGGAGG
ATGTGGGTTTACTCTTTGCCCGCCTTGGCAAGTACATTCTGTGCTGCCTGCTGGGTCACGCCATCCATGG
GCTCCTGGTACTGCCCCTCATCTACTTCCTCTTCACCCGCAAAAACCCCTACCGCTTCCTGTGGGGCATC
GTGACGCCGCTGGCCACTGCCTTTGGGACCTCTTCCAGTTCCGCCACGCTGCCGCTGATGATGAAGTGCG
TGGAGGAGAATAATGGCGTGGCCAAGCACATCAGCCGTTTCATCCTGCCCATCGGCGCCACCGTCAACAT
GGACGGTGCCGCGCTCTTCCAGTGCGTGGCCGCAGTGTTCATTGCACAGCTCAGCCAGCAGTCCTTGGAC
TTCGTAAAGATCATCACCATCCTGGTCACGGCCACAGCGTCCAGCGTGGGGGCAGCGGGCATCCCTGCTG
GAGGTGTCCTCACTCTGGCCATCATCCTCGAAGCAGTCAACCTCCCGGTCGACCATATCTCCTTGATCCT
GGCTGTGGACTGGCTAGTCGACCGGTCCTGTACCGTCCTCAATGTAGAAGGTGACGCTCTGGGGGCAGGA
CTCCTCCAAAATTATGTGGACCGTACGGAGTCGAGAAGCACAGAGCCTGAGTTGATACAAGTGAAGAGTG
AGCTGCCCCTGGATCCGCTGCCAGTCCCCACTGAGGAAGGAAACCCCCTCCTCAAACACTATCGGGGGCC
CGCAGGGGATGCCACGGTCGCCTCTGAGAAGGAATCAGTCATGTAAACCCCGGGAGGGACCTTCCCTGCC
CTGCTGGGGGTGCTCTTTGGACACTGGATTATGAGGAATGGATAAATGGATGAGCTAGGGCTCTGGGGGT
CTGCCTGCACACTCTGGGGAGCCAGGGGCCCCAGCACCCTCCAGGACAGGAGATCTGGGATGCCTGGCTG
CTGGAGTACATGTGTTCACAAGGGTTACTCCTCAAAACCCCCAGTTCTCACTCATGTCCCCAACTCAAGG
CTAGAAAACAGCAAGATGGAGAAATAATGTTCTGCTGCGTCCCCACCGTGACCTGCCTGGCCTCCCCTGT
CTCAGGGAGCAGGTCACAGGTCACCATGGGGAATTCTAGCCCCCACTGGGGGGATGTTACAACACCATGC
TGGTTATTTGGCGGCTGTAGTTGTGGGGGGATGTGTGTGTGCACGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGTGTTCTGTGACCTCCTGTCCCCATGGTACGTCCCACCCTGTCCCCAGATCCCCTATTCCCTC
CACAATAACAGAAACACTCCCAGGGACTCTGGGGAGAGGCTGAGGACAAATACCTGCTGTCACTCCAGAG
GACATTTTTTTAGCAATAAAATTGAGTGTCAACTATTTAAAAAAAAAAAAAAAAA

>gi|4507046|ref|NM_003045.1| Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 (SLC7A1), mRNA
CGATCCTGCCGGAGCCCCGCCGCCGCCGGCTTGGATTCTGAAACCTTCCTTGTATCCCTCCTGAGACATC
TTTGCTGCAAGATCGAGGCTGTCCTCTGGTGAGAAGGTGGTGAGGCTTCCCGTCATATTCCAGCTCTGAA
CAGCAACATGGGGTGCAAAGTCCTGCTCAACATTGGGCAGCAGATGCTGCGGCGGAAGGTGGTGGACTGT
AGCCGGGAGGAGACGCGGCTGTCTCGCTGCCTGAACACTTTGATCTGGTGGCCCTCGGGGTGGGCAGCA
CACTGGGTGCTGGTGTCTACGTCCTGGCTGGAGCTGTGGCCCGTGAGAATGCAGGCCCTGCCATTGTCAT
CTCCTTCCTGATCGCTGCGCTGGCCTCAGTGCTGGCTGGCCTGTGCTATGGCGAGTTTGGTGCTCGGGTC
CCCAAGACGGGCTCAGCTTACCTCTACAGCTATGTCACCGTTGGAGAGCTCTGGGCCTTCATCACCGGCT
GGAACTTAATCCTCTCCTACATCATCGGTACTTCAAGCGTAGCGAGGGCCTGGAGCGCCACCTTCGACGA
GCTGATAGGCAGACCCATCGGGGAGTTCTCACGGACACACATGACTCTGAACGCCCCCGGCGTGCTGGCT
GAAAACCCCGACATATTCGCAGTGATCATAATTCTCATCTTGACAGGACTTTTAACTCTTGGTGTGAAAG
AGTCGGCCATGGTCAACAAAATATTCACTTGTATTAACGTCCTGGTCCTGGGCTTCATAATGGTGTCAGG
ATTTGTGAAAGGATCGGTTAAAAACTGGCAGCTCACGGAGGAGGATTTTGGGAACACATCAGGCCGTCTC
TGTTTGAACAATGACACAAAAGAAGGGAAGCCCGGTGTTGGTGGATTCATGCCCTTCGGGTTCTCTGGTG
TCCTGTCGGGGGCAGCGACTTGCTTCTATGCCTTCGTGGGCTTTGACTGCATCGCCACCACAGGTGAAGA
GGTGAAGAACCCACAGAAGGCCATCCCCGTGGGGATCGTGGCGTCCCTCTTGATCTGCTTCATCGCCTAC
TTTGGGGTGTCGGCTGCCCTCACGCTCATGATGCCCTACTTCTGCCTGGACAATAACAGCCCCCTGCCCG
ACGCCTTTAAGCACGTGGGCTGGGAAGGTGCCAAGTACGCAGTGGCCGTGGGCTCCCTCTGCGCTCTTTC
CGCCAGTCTTCTAGGTTCCATGTTTCCCATGCCTCGGGTTATCTATGCCATGGCTGAGGATGGACTGCTA
TTTAAATTCTTAGCCAACGTCAATGATAGGACCAAAACACCAATAATCGCCACATTAGCCTCGGGTGCCG
TTGCTGCTGTGATGGCCTTCCTCTTTGACCTGAAGGACTTGGTGGACCTCATGTCCATTGGCACTCTCCT
GGCTTACTCGTTGGTGGCTGCCTGTGTGTTGGTCTTACGGTACCAGCCAGAGCAGCCTAACCTGGTATAC
CAGATGGCCAGTACTTCCGACGAGTTAGATCCAGCAGACCAAAATGAATTGGCAAGCACCAATGATTCCC
AGCTGGGGTTTTTACCAGAGGCAGAGATGTTCTCTTTGAAAACCATACTCTCACCCAAAAACATGGAGCC
TTCCAAAATCTCTGGGCTAATTGTGAACATTTCAACCAGCCTTATAGCTGTTCTCATCATCACCTTCTGC
ATTGTGACCGTGCTTGGAAGGGAGGCTCTCACCAAAGGGGCGCTGTGGGCAGTCTTTCTGCTCGCAGGGT
CTGCCCTCCTCTGTGCCGTGGTCACGGGCGTCATCTGGAGGCAGCCCGAGAGCAAGACCAAGCTCTCATT
TAAGGTTCCCTTCCTGCCAGTGCTCCCCATCCTGAGCATCTTCGTGAACGTCTATCTCATGATGCAGCTG
GACCAGGGCACCTGGGTCCGGTTTGCTGTGTGGATGCTGATAGGCTTCATCATCTACTTTGGCTATGGCC
TGTGGCACAGCGAGGAGGCGTCCCTGGATGCCGACCAAGCAAGGACTCCTGACGGCAACTTGGACCAGTG
CAAGTGACGCACAGCCCCGCCCCCCGGAGGTGGCAGCAGCCCCGAGGGACGCCCCCAGAGGACCGGGAGG
CACCCCACCCTCCCCACCAGTGCAACAGAAACCACCTGCGTCCACACCCTCACTGCA

>gi|4507048|ref|NM_003046.1| Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
GAATTCCGGCTCTCAAATTTTCTATAGAATCAAGATAGAACCTTTAGATGTCTCACCACGAAACTAGCAA
CTGGAATGAAGATAGAAACAAGTGGTTATAACTCAGACAAACTAATTTGTCGAGGGTTTATTGGAACACC
TGCCCCACCGGTTTGCGACANAAGTTTCTCCTGTCGCCTTCGTCAGACGTCAGAATGATTCCTTGCAGAG
CCGCGCTGACCTTTGCCCGATGTCTGATCCGGAGAAAAATCGTGACCCTGGACAGTCTAGAAGACACCAA
ATTATGCCGCTGCTTATCCACCATGGACCTCATTGCCCTGGGCGTTGGAAGCACCCTTGGGGCCGGGGTT
TATGTCCTCGCTGGGGAGGTGGCCAAGGCAGACTCGGGCCCCAGCATCGTGGTGTCCTTCCTCATTGCTG
CCCTGGCTTCAGTGATGGCTGGCCTCTGCTATGCCGAATTTGGGGCCCGTGTTCCCAAGACGGGGTCTGC
ATATTTGTACACCTACGTGACTGTCGGAGAGCTGTGGGCCTTCATCACTGGCTGGAATCTCATTTTATCG
TATGTGATAGGTACATCAAGTGTTGCAAGAGCCTGGAGTGGCACCTTTGATGAACTTCTTAGCAAACAGA
TTGGTCAGTTTTTGAGGACATACTTCAGAATGAATTACACTGGTCTTGCAGAATATCCCGATTTTTTTGC
TGTGTGCCTTATATTACTTCTAGCAGGTCTTTTGTCTTTTGGAGTAAAAGAGTCTGCTTGGGTGAATAAA
GTCTTCACAGCTGTTAATATTCTCGTCCTTCTGTTTGTGATGGTTGCTGGGTTTGTGAAAGGAAATGTGG
CAAACTGGAAGATTAGTGAAGAGTTTCTCAAAAATATATCAGCAAGTGCCAGAGAGCCACCTTCTGAAAA
CGGAACAAGTATCTATGGGGCTGGTGGCTTTATGCCTTATGGCTTTACGGGAACGTTGGCTGGTGCTGCA
ACTTGCTTTTATGCCTTTGTGGGATTTGACTGCATTGCAACAACTGGTGAAGAAGTTCGGAATCCCCAGA
AAGCTATTCCCATTGGAATTGTGACGTCTTTGCTTGTTTGCTTTATGGCCTATTTTGGGGTCTCTGCAGC
TTTAACACTTATGATGCCGTACTACCTCCTCGATGAAAAAAGCCCCCTTCCTGTAGCGTTTGAATATGTG
GGATGGGGTCCTGCCAAATATGTCGTCGCAGCTGGTTCTCTCTGCGCCTTGTCAACAAGTCTTCTGGGCT
CTATGTTTCCTTTACCCCGAATTCTGTTTGCCATGGCCCGGGATGGCTTACTGTTTAGATTTCTTGCCAG
AGTGAGTAAGAGGCAGTCACCAGTTGCTGCCACGTTGACTGCAGGGGTCATTTCTGCTTTGATGGCCTTT

CTGTTTGACCTGAAGGCGCTTGTGGACATGATGTCCATTGGCACACTCATGGCCTACTCTCTGGTGGCAG
CCTGTGTTCTCATCCTCAGGTACCAGCCTGGCTTATCTTACGACCAGCCCAAATGTTCTCCTGAGAAAGA
TGGTCTGGGATCGTCTCCCAGGGTAACCTCGAAGAGTGAGTCCCAGGTCACCATGCTGCAGAGACAGGGC
TTCAGCATGCGGACCCTCTTCTGCCCCTCCCTTCTGCCAACACAGCAGTCAGCTTCTCTCGTGAGCTTTC
TGGTAGGATTCCTAGCTTTCCTCGTGTTGGCCTGAGTGTCTTGACCACTTACGGAGTTCATGCCATCAC
CAGGCTGGAGGCCTGGAGCCTCGCTCTCCTCACGCTGTTTCTTGTTCTCTTCGTTGCCATCGTTCTCACC
ATCTGGAGGCAGCCCCAGAATCAGCAAAAAGTAGCCTTCATGGTTCCATTCTTACCATTTTTGCCAGCGT
TCAGCATCTTGGTGAACATTTACTTGATGGTCCAGTTAAGTGCAGACACTTGGGTCAGATTCAGCATTTG
GATGGCAATTGGCTTCCTGATTTACTTTTCTTATGGCATTAGACACAGCCTGGAGGGTCATCTGAGAGAT
GAAAACAATGAAGAAGATGCTTATCCAGACAACGTTCATGCAGCAGCAGAAGAAAAATCTGCCATTCAAG
CAAATGACCATCACCCAAGAAATCTCAGTTCACCTTTCATATTCCATGAAAAGACAAGTGAATTCTAACA
CTTGCAGGAGCAGAT

>gi|31543640|ref|NM_032803.3| Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (SLC7A3), mRNA
GCCTGAGCGGCCGAACTCGGCAGCTCCAACCCAACTCGGCTTAACTCCGCCTCACCGAGCCCAGTCCAAG
ACTCTGTGCTCCCTAGGTTTGCAACAGCTCTCTGATCATCTTCTTCAATTCCTGCTAGGATGCCGTGGCA
AGCATTTCGCAGATTTGGTCAAAAGCTGGTACGCAGACGTACACTGGAGTCAGGCATGGCTGAGACTCGC
CTTGCCAGATGCCTAAGCACCCTGGATTTAGTGGCCCTGGGTGTGGGCAGCACATTGGGTGCAGGCGTGT
ATGTCCTAGCTGGCGAGGTGGCCAAAGATAAAGCAGGGCCATCCATTGTGATCTGCTTTTTGGTGGCTGC
CCTGTCTTCTGTGTTGGCTGGGCTGTGCTATGCGGAGTTTGGTGCCCGGGTTCCCCGTTCTGGTTCGGCA
TATCTCTACAGCTATGTCACTGTGGGTGAACTCTGGGCCTTCACCACTGGCTGGAACCTCATCCTCTCCT
ATGTCATTGGTACAGCCAGTGTGGCCCGGGCCTGGAGCTCTGCTTTTGACAACCTGATTGGGAACCACAT
CTCTAAGACTCTGCAGGGGTCCATTGCACTGCACGTGCCCCATGTCCTTGCAGAATATCCAGATTTCTTT
GCTTTGGGCCTCGTGTTGCTGCTCACTGGATTGTTGGCTCTCGGGGCTAGTGAGTCGGCCCTGGTTACCA
GAGTGTTCACAGGCGTGAACCTTTTGGTTCTTGGGTTCGTCATGATCTCTGGCTTCGTTAAGGGGGACGT
GCACAACTGGAAGCTCACAGAAGAGGACTACGAATTGGCCATGGCTGAACTCAATGACACCTATAGCTTG
GGTCCTCTGGGCTCTGGAGGATTTGTGCCTTTCGGCTTCGAGGGAATTCTCCGTGGAGCAGCGACCTGTT
TCTATGCATTTGTTGGTTTCGACTGTATTGCTACCACTGGAGAAGAAGCCCAGAATCCCCAGCGTTCCAT
CCCGATGGGCATTGTGATCTCACTGTCTGTCTGCTTTTTGGCGTATTTTGCTGTCTCTTCTGCACTCACC
CTGATGATGCCTTACTACCAGCTTCAGCCTGAGAGCCCTTTGCCTGAGGCATTTCTCTACATTGGATGGG
CTCCTGCCCGCTATGTTGTGGCTGTTGGCTCCCTCTGTGCTCTTTCTACCAGCCTCCTGGGCTCCATGTT
CCCCATGCCTCGGGTGATCTACGCGATGGCAGAGGATGGCCTCCTGTTCCGTGTACTTGCTCGGATCCAC
ACCGGCACACGCACCCCAATCATAGCCACCGTGGTCTCTGGCATTATTGCAGCATTCATGGCATTCCTCT
TCAAACTCACTGATCTTGTGGACCTCATGTCAATTGGGACCCTGCTTGCTTACTCCCTGGTGTCGATTTG
TGTTCTCATCCTCAGGTATCAACCTGATCAGGAGACAAAGACTGGGGAAGAAGTGGAGTTGCAGGAGGAG
GCAATAACTACTGAATCAGAGAAGTTGACCCTATGGGGACTATTTTTCCCACTCAACTCCATCCCCACTC
CACTCTCTGGCCAAATTGTCTATGTTTGTTCCTCATTGCTTGCTGTCCTGCTGACTGCTCTTTGCCTGGT
GCTGGCCCAGTGGTCAGTTCCATTGCTTTCTGGAGACCTGGTGTGGACTGCAGTGGTTGTGCTGCTCCTG
CTGCTCATTATTGGGATCATTGTGGTCATCTGGAGACAGCCACAGAGCTCCACTCCCCTTCACTTTAAGG
TGCCTGCTTTGCCTCTCCTCCCACTAATGAGCATCTTTGTGAATATTTACCTTATGATGCAGATGACAGC
TGGTACCTGGGCCCGATTTGGGGTCTGGATGCTGATTGGCTTTGCTATCTACTTCGGCTATGGGATCCAG
CACAGCCTGGAAGAGATTAAGAGTAACCAACCCTCACGCAAGTCTAGAGCCAAAACTGTAGACCTTGATC
CCGGCACTCTCTATGTCCACTCAGTTTGACATCGTCACACCTAAATGCTGTCTGGTCCCCTGCACAATAA
TGGAGAGTACTCCTGACCCCAGTGACAGCTAGCCCTCCCCTGTGATGGTGGTGGTGGATACTAATACAGT
TCTGTACGATGTGAAGGATGTGTCTTTGCTATTTCTTGTCTATTTAACCCGTCTGCTTCTAAATGATGT
CTAGCTGCTTACCAACTTTAAAAAATGATATTAAAAGAAAGTAGAAAAATAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

>gi|29789099|ref|NM_018837.1| Homo sapiens similar to glucosamine-6-sulfatases (SULF2), mRNA
GGGCCATTTCTGGACAACAGCTGCTATTTTCACTTGAGCCCAAGTTAATTTCTCGGGGAGTTCTCGGGCG
CGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGGCGCCGGCCTCTCCAATGGCA
AATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTCGGCAAAGGCAGTCGAGTGTTTGCAGACCGGGGCGAG
TCCTGTGAAAGCAGATAAAAGAAAACATTTATTAACGTGTCATTACGAGGGGAGCGCCCGGCCGGGGCTG
TCGCACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCTAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGC
AGATTCACGTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCACGATATTTGATTT

ATTAGCGATGCCCCCTGGTTTGTGTGTTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTC
CCTCGTTTCCAGCTCCTGGGCGAATCCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGA
GTGTGTCGAATCTGCGAGTGAAGAGGGACGAGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCC
CGCATCCCAAAAGAAGCACCAGATCAGCAAAAAAAGAAGATGGGCCCCCCGAGCCTCGTGCTGTGCTTGC
TGTCCGCAACTGTGTTCTCCCTGCTGGGTGGAAGCTCGGCCTTCCTGTCGCACCACCGCCTGAAAGGCAG
GTTTCAGAGGGACCGCAGGAACATCCGCCCCAACATCATCCTGGTGCTGACGGACGACCAGGATGTGGAG
CTGGGTTCCATGCAGGTGATGAACAAGACCCGGCGCATCATGGAGCAGGGCGGGGCGCACTTCATCAACG
CCTTCGTGACCACACCCATGTGCTGCCCCTCACGCTCCTCCATCCTCACCGGCAAGTACGTCCACAACCA
CAACACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGCAGGCACAGCACGAGAGCCGCACCTTT
GCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATACAACGGCT
CCTACGTGCCACCCGGCTGGAAGGAGTGGGTCGGACTCCTTAAAAACTCCCGCTTTTATAACTACACGCT
GTGTCGGAACGGGGTGAAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCACAGACCTCATCACC
AATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCCTCATGGTCATCA
GCCATGCAGCCCCCCACGGCCCTGAGGATTCAGCCCCACAATATTCACGCCTCTTCCCAAACGCATCTCA
GCACATCACGCCGAGCTACAACTACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGCCC
ATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCCTCATGTCGGTGG
ACGACTCCATGGAGACGATTTACAACATGCTGGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATA
CACCGCCGACCACGGTTACCACATCGGCCAGTTTGGCCTGGTGAAAGGGAAATCCATGCCATATGAGTTT
GACATCAGGGTCCCGTTCTACGTGAGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCC
TCAACATTGACCTGGCCCCCACCATCCTGGACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAA
ATCCATCCTCAAGCTGCTGGACACGGAGCGGCCGGTGAATCGGTTTCACTTGAAAAAGAAGATGAGGGTC
TGGCGGGACTCCTTCTTGGTGGAGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCCC
AGGAGGAGAACTTTCTGCCCAAGTACCAGCGTGTGAAGGACCTGTGTCAGCGTGCTGAGTACCAGACGGC
GTGTGAGCAGCTGGGACAGAAGTGGCAGTGTGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGC
AAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCCTCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCA
GCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTCAGCCTGGCCGGACGCCGGAAAAAACTCTTCAA
GAAGAAGTACAAGGCCAGCTATGTCCGCAGTCGCTCCATCCGCTCAGTGGCCATCGAGGTGGACGGCAGG
GTGTACCACGTAGGCCTGGGTGATGCCGCCCAGCCCCGAAACCTCACCAAGCGGCACTGGCCAGGGGCCC
CTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGCCTTCCCGACTACTCAGCCGC
CAACCCCATTAAAGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCAGTGTGACCTGGACCTG
TACAAGTCCCTGCAGGCCTGGAAAGACCACAAGCTGCACATCGACCACGAGATTGAAACCCTGCAGAACA
AAATTAAGAACCTGAGGGAAGTCCGAGGTCACCTGAAGAAAAAGCGGCCAGAAGAATGTGACTGTCACAA
AATCAGCTACCACACCCAGCACAAAGGCCGCCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTCAGGAAG
GGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAAACTCCGCAAGCTGC
TCAAGCGCCTGCAGAACAACGACACGTGCAGCATGCCAGGCCTCACGTGCTTCACCCACGACAACCAGCA
CTGGCAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCCTGCACCAGCGCCAACAATAACACGTAC
TGGTGCATGAGGACCATCAATGAGACTCACAATTTCCTCTTCTGTGAATTTGCAACTGGCTTCCTAGAGT
ACTTTGATCTCAACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCCTCAA
CCAGCTACACGTACAGCTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCGGACTCGA
AACATGGACCTGGGACTTAAAGATGGAGGAAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGGC
CAGAAATGAAGAGACCTTCTTCCAAATCACTGGGACAACTGTGGGAAGGCTGGGAAGGTTAAGAAACAAC
AGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGACTGCACAGGCAATGAAAAACCATGTGGGTGATT
TCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGCAAGCACGCACTCTCAGTCAACATGACAGA
TTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCCATTTTTGCCCCTGCTTTTGCTTTGG
ATTATACCTCACCAGCTGCACAAAATGCATTTTTTCGTATCAAAAAGTCACCACTAACCCTCCCCCAGAA
GCTCACAAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCCTTGGAAATTTCTCCCAAGGGCGAAAGTC
ATTGGAATTTTTAAATCATAGGGGAAAAGCAGTCCTGTTCTAAATCCTCTTATTCTTTTGGTTTGTCACA
AAGAAGGAACTAAGAAGCAGGACAGAGGCAACGTGGAGAGGCTGAAAACAGTGCAGAGACGTTTGACAAT
GAGTCAGTAGCACAAAAGAGATGACATTTACCTAGCATATAAACCCTGGTTGCCTCTGAAGAAACTGCCT
TCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACTTTTAGGGGAACCTAATAAGAAATCC
CAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAAAGAAAAAAAAAAAAAATTGTG
GACATTTCTGTTCCTGTCCAGATACCATTTCTCCTAGTATTTCTTTGTTATGTCCCAGAACTGATGTTTT
TTTTTTAAGGTACTGAAAAGAAATGAAGTTGATGTATGTCCCAAGTTTTGATGAAACTGTATTTGTAAAA
AAAATTTTGTAGTTTAAGTATTGTCATACAGTGTTCAAAACCCCAGCCAATGACCAGCAGTTGGTATGAA
GAACCTTTGACATTTTGTAAAAGGCCATTTCTTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAA

>gi|29789063|ref|NM_015170.1| Homo sapiens sulfatase 1 (SULF1), mRNA
GGAGTTCTCAGACCTCCAGTTTCAGCCCTGCCCTCAGCCTCCAATCCGTAAGAGACACCCAGCCCCAGCA
ATTGGATTGGGCAGCCCGTCTTGACACACCACTGTGCTGAGTGCTTGAGGACGTGTTTCAACAGATGGTT
GGGGTTAGTGTGTGTCATCACATTCGAGTGGGATTAAGAGAAGGAAGGCTGCCTTGCTGGAGCTGTGTG
GTCTTCTCCAAGTGAGAGTCGCAGGCAATAGAACTACTTTGCTTTTGGAGGAAAAGGAGGAATTCATTTT
CAGCAGACACAAGAAAAGCAGTTTTTTTTCAGGGATTCTTCACTTCTCTTGAACAAGGAACTCACTCAG
AGACTAACACAAAGGAAGTAATTTCTTACCTGGTCATTATTTAGTCTACAATAAGTTCATCCTTCTTCAG
TGTGACCAGTAAATTCTTCCCATACTCTTGAAGAGAGCATAATTGGAATGGAGAGGTGGTGCTGACGGCC
ACCCACCATCATCTAAAGAAGATAAACTTGGCAAATGACATGCAGGTTCTTCAAGGCAGAATAATTGCAG
AAAATCTTCAAAGGACCCTATCTGCAGATGTTCTGAATACCTCTGAGAATAGAGATTGATTATTCAACCA
GGATACCTAATTCAAGAACTCCAGAAATCAGGAGACGGAGACATTTTGTCAGTTTTGCAACATTGGACCA
AATACAATGAAGTATTCTTGCTGTGCTCTGGTTTTGGCTGTCCTGGGCACAGAATTGCTGGGAAGCCTCT
GTTCGACTGTCAGATCCCCGAGGTTCAGAGGACGGATACAGCAGGAACGAAAAAACATCCGACCCAACAT
TATTCTTGTGCCTACCGATGATCAAGATGTGGAGCTGGGGTCCCTGCAAGTCATGAACAAAACGAGAAAG
ATTATGGAACATGGGGGGCCACCTTCATCAATGCCTTTGTGACTACACCCATGTGCTGCCCGTCACGGT
CCTCCATGCTCACCGGGAAGTATGTGCACAATCACAATGTCTACACCAACAACGAGAACTGCTCTTCCCC
CTCGTGGCAGGCCATGCATGAGCCTCGGACTTTTGCTGTATATCTTAACAACACTGGCTACAGAACAGCC
TTTTTTGGAAAATACCTCAATGAATATAATGGCAGCTACATCCCCCCTGGGTGGCGAGAATGGCTTGGAT
TAATCAAGAATTCTCGCTTCTATAATTACACTGTTTGTCGCAATGGCATCAAAGAAAAGCATGGATTTGA
TTATGCAAAGGACTACTTCACAGACTTAATCACTAACGAGAGCATTAATTACTTCAAAATGTCTAAGAGA
ATGTATCCCCATAGGCCCGTTATGATGGTGATCAGCCACGCTGCGCCCCACGGCCCCGAGGACTCAGCCC
CACAGTTTTCTAAACTGTACCCCAATGCTTCCCAACACATAACTCCTAGTTATAACTATGCACCAAATAT
GGATAAACACTGGATTATGCAGTACACAGGACCAATGCTGCCCATCCACATGGAATTTACAAACATTCTA
CAGCGCAAAAGGCTCCAGACTTTGATGTCAGTGGATGATTCTGTGGAGAGGCTGTATAACATGCTCGTGG
AGACGGGGGAGCTGGAGAATACTTACATCATTTACACCGCCGACCATGGTTACCATATTGGGCAGTTTGG
ACTGGTCAAGGGGAAATCCATGCCATATGACTTTGATATTCGTGTGCCTTTTTTTATTCGTGGTCCAAGT
GTAGAACCAGGATCAATAGTCCCACAGATCGTTCTCAACATTGACTTGGCCCCCACGATCCTGGATATTG
CTGGGCTCGACACACCTCCTGATGTGGACGGCAAGTCTGTCCTCAAACTTCTGGACCCAGAAAAGCCAGG
TAACAGGTTTCGAACAAACAAGAAGGCCAAAATTTGGCGTGATACATTCCTAGTGGAAAGAGGCAAATTT
CTACGTAAGAAGGAAGAATCCAGCAAGAATATCCAACAGTCAAATCACTTGCCCAAATATGAACGGGTCA
AAGAACTATGCCAGCAGGCCAGGTACCAGACAGCCTGTGAACAACCGGGGCAGAAGTGGCAATGCATTGA
GGATACATCTGGCAAGCTTCGAATTCACAAGTGTAAAGGACCCAGTGACCTGCTCACAGTCCGGCAGAGC
ACGCGGAACCTCTACGCTCGCGGCTTCCATGACAAAGACAAAGAGTGCAGTTGTAGGGAGTCTGGTTACC
GTGCCAGCAGAAGCCAAAGAAAGAGTCAACGGCAATTCTTGAGAAACCAGGGGACTCCAAAGTACAAGCC
CAGATTTGTCCATACTCGGCAGACACGTTCCTTGTCCGTCGAATTTGAAGGTGAAATATATGACATAAAT
CTGGAAGAAGAAGAAGAATTGCAAGTGTTGCAACCAAGAAACATTGCTAAGCGTCATGATGAAGGCCACA
AGGGGCCAAGAGATCTCCAGGCTTCCAGTGGTGGCAACAGGGGCAGGATGCTGGCAGATAGCAGCAACGC
CGTGGGCCCACCTACCACTGTCCGAGTGACACACAAGTGTTTTATTCTTCCCAATGACTCTATCCATTGT
GAGAGAGAACTGTACCAATCGGCCAGAGCGTGGAAGGACCATAAGGCATACATTGACAAAGAGATTGAAG
CTCTGCAAGATAAAATTAAGAATTTAAGAGAAGTGAGAGGACATCTGAAGAGAAGGAAGCCTGAGGAATG
TAGCTGCAGTAAACAAAGCTATTACAATAAAGAGAAAGGTGTAAAAAAGCAAGAGAAATTAAAGAGCCAT
CTTCACCCATTCAAGGAGGCTGCTCAGGAAGTAGATAGCAAACTGCAACTTTTCAAGGAGAACAACCGTA
GGAGGAAGAAGGAGAGGAAGGAGAAGAGACGGCAGAGGAAGGGGGAAGAGTGCAGCCTGCCTGGCCTCAC
TTGCTTCACGCATGACAACAACCACTGGCAGACAGCCCCGTTCTGGAACCTGGGATCTTTCTGTGCTTGC
ACGAGTTCTAACAATAACACCTACTGGTGTTTGCGTACAGTTAATGAGACGCATAATTTTCTTTTCTGTG
AGTTTGCTACTGGCTTTTTGGAGTATTTTGATATGAATACAGATCCTTATCAGCTCACAAATACAGTGCA
CACGGTAGAACGAGGCATTTTGAATCAGCTACACGTACAACTAATGGAGCTCAGAAGCTGTCAAGGATAT
AAGCAGTGCAACCCAAGACCTAAGAATCTTGATGTTGGAAATAAAGATGGAGGAAGCTATGACCTACACA
GAGGACAGTTATGGGATGGATGGGAAGGTTAATCAGCCCCGTCTCACTGCAGACATCAACTGGCAAGGCC
TAGAGGAGCTACACAGTGTGAATGAAAACATCTATGAGTACAGACAAAACTACAGACTTAGTCTGGTGGA
CTGGACTAATTACTTGAAGGATTTAGATAGAGTATTTGCACTGCTGAAGAGTCACTATGAGCAAAATAAA
ACAAATAAGACTCAAACTGCTCAAAGTGACGGGTTCTTGGTTGTCTCTGCTGAGCACGCTGTGTCAATGG
AGATGGCCTCTGCTGACTCAGATGAAGACCCAAGGCATAAGGTTGGGAAAACACCTCATTTGACCTTGCC
AGCTGACCTTCAAACCCTGCATTTGAACCGACCAACATTAAGTCCAGAGAGTAAACTTGAATGGAATAAC
GACATTCCAGAAGTTAATCATTTGAATTCTGAACACTGGAGAAAAACCGAAAAATGGACGGGGCATGAAG
AGACTAATCATCTGGAAACCGATTTCAGTGGCGATGGCATGACAGAGCTAGAGCTCGGGCCCAGCCCCAG
GCTGCAGCCCATTCGCAGGCACCCGAAAGAACTTCCCCAGTATGGTGGTCCTGGAAAGGACATTTTGAA

GATCAACTATATCTTCCTGTGCATTCCGATGGAATTTCAGTTCATCAGATGTTCACCATGGCCACCGCAG
AACACCGAAGTAATTCCAGCATAGCGGGGAAGATGTTGACCAAGGTGGAGAAGAATCACGAAAAGGAGAA
GTCACAGCACCTAGAAGGCAGCGCCTCCTCTTCACTCTCCTCTGATTAGATGAAACTGTTACCTTACCCT
AAACACAGTATTTCTTTTTAACTTTTTTATTTGTAAACTAATAAAGGTAATCACAGCCACCAACATTCCA
AGCTACCCTGGGTACCTTTGTGCAGTAGAAGCTAGTGAGCATGTGAGCAAGCGGTGTGCACACGGAGACT
CATCGTTATAATTTACTATCTGCCAAGAGTAGAAAGAAAGGCTGGGGATATTTGGGTTGGCTTGGTTTTG
ATTTTTTGCTTGTTTGTTTGTTTTGTACTAAAACAGTATTATCTTTTGAATATCGTAGGGACATAAGTAT
ATACATGTTATCCAATCAAGATGGCTAGAATGGTGCCTTTCTGAGTGTCTAAAACTTGACACCCCTGGTA
AATCTTTCAACACACTTCCACTGCCTGCGTAATGAAGTTTTGATTCATTTTTAACCACTGGAATTTTTCA
ATGCCGTCATTTTCAGTTAGATGATTTTGCACTTTGAGATTAAAATGCCATGTCTATTTGATTAGTCTTA
TTTTTTTATTTTTACAGGCTTATCAGTCTCACTGTTGGCTGTCATTGTGACAAAGTCAAATAAACCCCCA
AGGACGACACACAGTATGGATCACATATTGTTTGACATTAAGCTTTTGCCAGAAAATGTTGCATGTGTTT
TACCTCGACTTGCTAAAATCGATTAGCAGAAAGGCATGGCTAATAATGTTGGTGGTGAAAATAAATAAAT
AAGTAAACAAAATGAAGATTGCCTGCTCTCTCTGTGCCTAGCCTCAAAGCGTTCATCATACATCATACCT
TTAAGATTGCTATATTTTGGGTTATTTTCTTGACAGGAGAAAAAGATCTAAAGATCTTTTATTTTCATCT
TTTTTGGTTTTCTTGGCATGACTAAGAAGCTTAAATGTTGATAAAATATGACTAGTTTTGAATTTACACC
AAGAACTTCTCAATAAAAGAAAATCATGAATGCTCCACAATTTCAACATACCACAAGAGAAGTTAATTTC
TTAACATTGTGTTCTATGATTATTTGTAAGACCTTCACCAAGTTCTGATATCTTTTAAAGACATAGTTCA
AAATTGCTTTTGAAAATCTGTATTCTTGAAAATATCCTTGTTGTGTATTAGGTTTTTAAATACCAGCTAA
AGGATTACCTCACTGAGTCATCAGTACCCTCCTATTCAGCTCCCCAAGATGATGTGTTTTTGCTTACCCT
AAGAGAGGTTTTCTTCTTATTTTTAGATAATTCAAGTGCTTAGATAAATTATGTTTTCTTTAAGTGTTTA
TGGTAAACTCTTTTAAAGAAAATTTAATATGTTATAGCTGAATCTTTTTGGTAACTTTAAATCTTTATCA
TAGACTCTGTACATATGTTCAAATTAGCTGCTTGCCTGATGTGTGTATCATCGGTGGGATGACAGAACAA
ACATATTTATGATCATGAATAATGTGCTTTGTAAAAAGATTTCAAGTTATTAGGAAGCATACTCTGTTTT
TTAATCATGTATAATATTCCATGATACTTTTATAGAACAATTCTGGCTTCAGGAAAGTCTAGAAGCAATA
TTTCTTCAAATAAAAGGTGTTTAAACTTT

>gi|27597095|ref|NM_173355.1| Homo sapiens uridine phosphorylase-2 (UPase-2), mRNA
GCCGCGCGGCACGGGTGAGTGCCCAGGGACTTCACCAGTGCTGCCATGCTGGCCCCAGGCTGTGAGTTGG
ACCCAGACCAAGAAGTGGTGAGGACAAGGCCTGAAGATGTGCCTGCTTCCCATTCAACTTCCACCATGAT
TGTAAGTGTCCTGAGGCCTCCCAGCCATGCTTCCTGTACAGCCTGTGGAACTGTGACTTTTCACATAGTA
GAGAGAATGGCTTCAGTTATACCTGCCTCCAATAGGTCCATGAGATCTGACAGGAATACATATGTTGGAA
AAAGGTTTGTTCACGTTAAAAATCCTTACTTGGATTTGATGGATGAAGACATTCTCTATCACTTGGATTT
GGGAACAAAAACACACAACCTACCAGCAATGTTTGGAGATGTAAAGTTTGTCTGTGTCGGTGGGAGCCCC
AACAGAATGAAAGCATTTGCACTGTTTATGCACAAGGAGCTCGGGTTTGAGGAAGCTGAAGAAGACATAA
AAGACATCTGTGCTGGGACAGACAGATACTGTATGTACAAAACCGGGCCTGTGCTCGCCATCAGTCACGG
CATGGGCATCCCCTCCATTTCTATTATGCTTCATGAACTCATCAAATTACTCCACCATGCACGGTGCTGC
GATGTCACCATTATTAGAATCGGTACATCAGGGGGAATAGGGATTGCACCAGGGACTGTTGTAATAACGG
ATATAGCTGTAGACTCCTTCTTTAAGCCCCGGTTTGAACAGGTCATTTTGGACAACATTGTCACCCGAAG
TACTGAACTGGACAAAGAACTGTCTGAAGAACTGTTCAACTGTAGCAAAGAAATCCCCAACTTCCCAACC
CTCGTTGGACATACAATGTGTACCTATGATTTTTATGAAGGCCAAGGCCGACTAGATGGAGCACTGTGCT
CCTTTTCCAGAGAAAAAAAGTTAGACTACTTGAAGAGAGCATTTAAAGCTGGTGTCAGGAATATTGAAAT
GGAATCTACAGTGTTTGCAGCTATGTGTGGACTCTGTGGTCTAAAAGCTGCTGTGGTCTGTGTGACACTT
CTCGACAGACTCGACTGTGATCAGATCAACTTGCCTCATGATGTCCTGGTGGAGTACCAGCAACGGCCTC
AGCTCCTAATCTCCAACTTCATCAGACGGCGGCTTGGACTTTGTGACTAGACGTCCTAACTGGGCAGCCC
AACCCTCCCCTGCAAGTTTGTAGCTCAAGTTGTAATGTGAAAGTCATATTTTATTTGTGGCATTTTTATA
TAGTTCTCATCCACATGCTAAATGGAAAGACTTTATGAAATCCTTCTCTCTTAAAAAGGAATTTATTGTA
AAAGAATACTCACACTAAATTAAATTCAAATTTCATTTTAGAATAAGTTAACTAAATCAGTCTAATAATT
AAAATTTTAAAACTCCTGGATTATGACATTTGGAGTTTCATATGCAGCATTAATTAAGCTCACATCAAAA
TAGACCAGCCATTTGCACATAGTTACCAGTCACTCTGTTTCTGAAACCAATCCAGAAATTCATGTTAGAA
CATTGTCAGGCACTTCTAGGTATTGGACAAGTGACAGAAACTGATCATCCATATTCAAAATATTTACAGA
AAAAAGTGTCAGTGAAATGTAGGTCTATATGGAAAAGTTACCATTAGGAAAATATGGCCATACTGCTTTT
TTACCCCTGCACTATTTCAGTGCACCACAGAATAGGATTCGAGATTTACATATGCCTGTTTGTGATTTTA
TCTCAGAATATAACAACTCTGGATTACATTTTCCTCTCAACTGAAAACCCTCAGTAATGCAAAGAAAGGC
CTTCCTTTTTCTTCAGAATCACAAGTGACTAAATTGCCTTCTAGCCATTTTTTCTTGTAAAAAAAGTGTT
TTGAGGAGGCTGTATTTTTTATTCCATTTCAATATTAACCAAATAGGCTGAGAAATTCATAGCAATTGAA

TTAAGACTTGAGTTCAAGATGTTAAAGGAATCCTTTTGTATGACTTGTCCAGACCGGCCTATTGCCCTAC
CCGTTTGATTCTCTGGGAGGCATGGTGCTCCTCCTGGCTGCACATGCTCTCTGTGAACTGATCGCATCTT
GGGTTCTTCTCAATTTGACATACTTGGGAGTCGGAATGACTGGATGGGGATGGGTAGAGGATGACTGGC
ACACTTGTATAGTATGTAATGTTGTGTACATATTATTTATATGGTTGTGGCTCAAATAAAGTTTAATTCC
AACACAAAAAAAAAAAAAAAA

>gi|31742506|ref|NM_003364.2| Homo sapiens uridine phosphorylase (UP), transcript variant 1, mRNA
GGTCAGCTGAGTTCGCCGGCCCAGGGCAGGCGGGGCCCGAGCCTAGCGGTAACCCCCGGGCAGGGCGGGG
CCGCTCGCAGACTCCATATGAGATTCACCTCGCAGGTGGTTCCCTCATTCGAGTGCTCCGGCGCACAGAC
CCGCGCCCCGCCGTCTGCGAGCCTCCCGAGAGCCGTCCCTTCGTCCGGCCCTGGAGCATTGCGTTTGTCG
CCGGTGTCGCAGTGCGAGGATGGCGCCGCGGGTGTAGCGGCTCTCTGCGCAGGCCGAGTGGGCCCAGAGA
AGCGAGGAACTCCGCAGCTCGTCGACACGTCTCGTCTCCTGTCCCAATTCAGGGCTTGGTGAGGTGACTC
GCGGTCGCGGGTGACTCGCCGGCAGGACACTGCCTGGAACGCCTGGAGCGCCTCCCACTGCAGACGTCTG
TCCGCCTCCAGCCGCTCTCCTCTGACGGGTCCTGCCTCAGTTGGCGGAATGGCGGCCACGGGAGCCAATG
CAGAGAAAGCTGAAAGTCACAATGATTGCCCCGTCAGACTTTTAAATCCAAACATAGCAAAAATGAAAGA
AGATATTCTCTATCATTTCAATCTCACCACTAGCAGACACAATTTCCCAGCCTTGTTTGGAGATGTGAAG
TTTGTGTGTGTTGGTGGAAGCCCCTCCCGGATGAAAGCCTTCATCAGGTGCGTTGGTGCAGAGCTGGGCC
TTGACTGCCCAGGTAGAGACTATCCCAACATCTGTGCGGGAACTGACCGCTATGCCATGTATAAAGTAGG
ACCGGTGCTGTCTGTCAGTCATGGTATGGGCATTCCTTCTATCTCAATCATGTTGCATGAGCTCATAAAG
CTGCTGTACTATGCCCGGTGCTCCAACGTCACTATCATCCGCATTGGCACTTCTGGTGGGATAGGTCTGG
AGCCCGGCACTGTGGTCATAACAGAGCAGGCAGTGGATACCTGCTTCAAGGCAGAGTTTGAGCAGATTGT
CCTGGGGAAGCGGGTCATCCGGAAAACGGACCTTAACAAGAAGCTGGTGCAGGAGCTGTTGCTGTGTTCT
GCAGAGCTGAGCGAGTTCACCACAGTGGTGGGGAACACCATGTGCACCTTGGACTTCTATGAAGGGCAAG
GCCGTCTGGATGGGGCTCTCTGCTCCTACACGGAGAAGGACAAGCAGGCGTATCTGGAGGCAGCCTATGC
AGCCGGCGTCCGCAATATCGAGATGGAGTCCTCGGTGTTTGCCGCCATGTGCAGCGCCTGCGGCCTCCAA
GCGGCCGTGGTGTGTGTCACCCTCCTGAACCGCCTGGAAGGGGACCAGATCAGCAGCCCTCGCAATGTGC
TCAGCGAGTACCAGCAGAGGCCGCAGCGGCTGGTGAGCTACTTCATCAAGAAGAAACTGAGCAAGGCCTG
AGCGCTGCCCTGCACCTCCGCAGACCTGCTGTGATGACTTGCCATTAAAAGCATTGTCCAAAATCCCCTG
TTGTGTGGACTTTGAGCACACTTTACACAAGAATCTAGAAAATCAGATCGCGATTAAGAGACAGAGAATC
TTGGATTAACCGCATGGGAGATGTTCTTCCTTTTGAAGTTTCATTGGAGCATTTTCAATGATGTTAGCCT
GATTTGGGGTTTCTTCAAGAACATTCTACCAAATTTTTGTACTATTTCTAGGGAAATTTTTCAGACTTTA
AAATTCTAATGGTAGTCAGATTTCATGTCACTAAACAAGAAATCTGACAATAGTGCCAGGAAACTAATTT
CCTGATACATTAAAAAAATTCCATGCAAAAAAAAAAAAAAAAAAAA

>gi|20127508|ref|NM_006834.2| Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA
GGGGGCCGCGAGCACTGGCGGGTTCTGGGTCCTGTGACCGGTCAGGCGGCGTCAGCGGGCGCGGCGGAGG
GCTGGCCGGCCTCGGGGGAGTTTCCGCGGCCGCCGGGGGCGCGGCGGCAGAGCGCGAGGCCGGGCAGGGG
GCCAGACTCGGAGTCGAGGCGCGCCCGACAGCCGCAGCGCTCATGGCGGGCGGAGGAGCCGGGGACCCCG
GCCTGGGGGCGGCCGCCGCCCCAGCGCCCGAGACCCGCGAGCACCTCTTCAAGGTGCTGGTGATCGGCGA
GCTTGGCGTGGGCAAGACCAGCATCATCAAGCGCTACGTCCACCAGCTCTTCTCCCAGCACTACCGGGCC
ACCATCGGGGTGGACTTCGCCCTCAAGGTCCTCAACTGGGACAGCAGGACTCTGGTGCGCCTGCAGCTGT
GGGACATCGCGGGGCAGGAGCGATTTGGCAACATGACCCGAGTATACTACAAGGAAGCTGTTGGTGCTTT
TGTAGTCTTTGATATATCAAGAAGTTCCACATTTGAGGCAGTCTTAAAATGGAAAAGTGATCTGGATAGT
AAAGTTCATCTTCCAAATGGCAGCCCTATCCCTGCTGTCCTCTTGGCTAACAAATGTGACCAGAACAAGG
ACAGTAGCCAGAGTCCTTCCCAGGTGGACCAATTCTGCAAAGAACATGGCTTTGCCGGATGGTTTGAAAC
CTCTGCAAAGGATAACATAAACATAGAGGAAGCTGCCCGGTTCCTAGTGGAGAAGATTCTTGTAAACCAC
CAAAGCTTTCCTAATGAAGAAAACGATGTGGACAAAATTAAGCTAGATCAAGAGACCTTGAGAGCAGAGA
ACAAATCCCAGTGTTGCTGATATATGGCTTCTGCTTCTCTTGTGTGTGCCTCAGCTCTGAAGAAGTTCCT
GAGAATGGGTTACAGATGTCATGTTAGCTGGGAGTCTTCCCACATGTGGCACTTCAAAAGGCAGCACCAC
TGGGCGCCTGCACTTATTTGAAAATGGAACTTTGGGAGAAGTATCCCTGCTAGTGGCTCTGTAACTTAAC
AGATGACAATTAGGCTTTTGTCATTGTTGCCATCATATGGAAGATAATGTTTACATCCTTTTAAACATTT
TTATATGACAATTCCTCAGGATTTGGTAAGGCTTCCAAGTTGTAGCTTTTAGTGTAAGTGCTGGGGTGGT
AATAAAATGTTACCTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

>gi|11641236|ref|NM_022337.1| Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA
GGCTGCGCTTCCCTGGTCAGGCACGGCACGTCTGGCCGGCCGCCAGGATGCAGGCCCCGCACAAGGAGCA
CCTGTACAAGTTGCTGGTGATTGGCGACCTGGGCGTGGGGAAGACCAGTATCATCAAGCGCTACGTGCAC
CAGAACTTCTCCTCGCACTACCGGGCCACAATCGGCGTGGACTTCGCGCTCAAGGTGCTCCACTGGGACC
CGGAGACTGTGGTGCGCCTGCAGCTCTGGGATATCGCAGGTCAAGAAAGATTTGGAAACATGACGAGGGT
CTATTACCGAGAAGCTATGGGTGCATTTATTGTCTTCGATGTCACCAGGCCAGCCACATTTGAAGCAGTG
GCAAAGTGGAAAAATGATTTGGACTCCAAGTTAAGTCTCCCTAATGGCAAACCGGTTTCAGTGGTTTTGT
TGGCCAACAAATGTGACCAGGGGAAGGATGTGCTCATGAACAATGGCCTCAAGATGGACCAGTTCTGCAA
GGAGCACGGTTTCGTAGGATGGTTTGAAACATCAGCAAAGGAAAATATAAACATTGATGAAGCCTCCAGA
TGCCTGGTGAAACACATACTTGCAAATGAGTGTGACCTAATGGAGTCTATTGAGCCGGACGTCGTGAAGC
CCCATCTCACATCAACCAAGGTTGCCAGCTGCTCTGGCTGTGCCAAATCCTAGTAGGCACCTTTGCTGGT
GTCTGGTAGGAATGACCTCATTGTTCCACAAATTGTGCCTCTATTTTTACCATTTTGGGTAAACGTCAGG
ATAGATATACCACATGTGGCAAGCCAAAGATCTATGCCTCTGTTTTTTCAATGAGAGAGAAATAGCAAAT
GTTCTTTCTATGCTTTCCTCACCATCATCACAGTGTTTACAAACTTTTGAAAATATTTAGTCTGTTACAA
ACTTCTGTCATGTAGCTGACCAAAATCCTGCAGGGCCACAGTCGGCACTGTTATTTGCTTCTTTTAATCA
GCAAAGGCCTCAAGTCTTAAAATAAAAGGGGAGAAGAACAAACTAGCTGTCAAGTCAAGGACTGGCTTTC
ACCTTGCCCTGGTGTCTTTTTCCAGATTTCAATATATTCTCTGATGGCCTGACAGGCCTATTAAGTAGAT
GTGATATTTTCTTCCAAGATGACCTCCATTCTCGGCAGACCTAAGAGTTGCCTCTGAGTTAGCTCTTTGG
AATCGTGAACACAGGTGTGCTATATTGTCCTTGTCCTAACTGTCACTTGCCATGGCCTGAATGTTGGCTT
AACTGAATATTGTATGAAAAGACATGCCTCCATATGTGCCTTTCTGTTAGCTCTCTTTGACTCAAGCTGT
GGGGCTCCTCTATACATGCTATACATGTAATATATATTATATATATTTTTGCAAGTGAACAATAAAACAT
TAAAAGATAAAA

>gi|4506374|ref|NM_003929.1| Homo sapiens RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA
CCACACTTCCCGCCTCCCTAAAACGCACACCCCGCTAGCCATGGGCAGCCGCGACCACCTGTTCAAAGTG
CTGGTGGTGGGGGACGCCGCAGTGGGCAAGACGTCGCTGGTGCAGCGATATTCCCAGGACAGCTTCAGCA
AACACTACAAGTCCACGGTGGGAGTGGATTTTGCTCTGAAGGTTCTCCAGTGGTCTGACTACGAGATAGT
GCGGCTTCAGCTGTGGGATATTGCAGGGCAGGAGCGCTTCACCTCTATGACACGATTGTATTATCGGGAT
GCCTCTGCCTGTGTTATTATGTTTGACGTTACCAATGCCACTACCTTCAGCAACAGCCAGAGGTGGAAAC
AGGACCTAGACAGCAAGCTCACACTACCCAATGGAGAGCCGGTGCCCTGCCTGCTCTTGGCCAACAAGTG
TGATCTGTCCCCTTGGGCAGTGAGCCGGGACCAGATTGACCGGTTCAGTAAAGAGAACGGTTTCACAGGT
TGGACAGAAACATCAGTCAAGGAGAACAAAAATATTAATGAGGCTATGAGAGTCCTCATTGAAAAGATGA
TGAGAAATTCCACAGAAGATATCATGTCTTTGTCCACCCAAGGGGACTACATCAATCTACAAACCAAGTC
CTCCAGCTGGTCCTGCTGCTAGTAGTGTTTGGCTTATTTTCCATCCCAGTTCTGGGAGGTCTTTTAAGTC
TCTTCCCTTTGGTTGCCCACCTGACCATTTTATTAAGTACATTTGAATTGTCTCCTGACTACTGTCCAGT
AAGGAGGCCCATTGTCACTTAGAAAAGACACCTGGAACCCATGTGCATTTCTGCATCTCCTGGATTAGCC
TTTCACATGTTGCTGACTCACATTAGTGCCAGTTAGTGCCTTCGGTGTAAGATCTTCTCATCAGCCCTCA
ATTTGTGATCCGGAATTTTGTGAGAAGGATTAGAAATCAGCACCTGCGTTTTAGAGATCATAATTCTCAC
CTACTTCTGAGCTTATTTTTCCATTTGATATTCATTGATATCATGACTTCCAATTGAGAGGAAAATGAGA
TCAAATGTCATTTCCCAAATTTCTTGTAGGCCGTTGTTTCAGATTCTTTCTGTCTTGGAATGTAAACATC
TGATTCTGGAATGCAGAAGGAGGGGTCTGGGCATCTGTGGATTTTTGGCTACTAGAAGTGTCCCAGAAGT
CACTGTATTTTTGAAACTTCTAACGTCATAATTAAGTTTCTCTTGTCTTGGCATCAAGAATAGTCAAGTT
TTTTGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTGGGGAGGCCAAGGCAGGCGGATCACAT
GAGGCCAGGAATTCGAGACCAACCTGGTCAGCATGGCAAAACCCCGTCTCTACTAAAAGTACAAAAATTA
GCCAGGCGTGATGGCACGTGTCTGTAATCCCAGCTACTCTGGAGACTGAGGTGGGAGAATCGCTTGAGAC
TGGGAGGCAGAGGTTGCAGTGAACCGAGATCATGCCACCGCACTTCAGCCTGGGTGACAGAGAAGGACTC
CGTCTCAAAAAAAAAAGAAAAAAGAATAGTCATTTTTAAACTACCTATCTCATGCAATGAAAGCATTTTC
TTCCACAAAGAGCTTAATCCTCATGATAGGATTGCCTAGTGTCTCCCATTTGCAGGTTTCTGGGTTGATG
TCTTAATGCATAATACTGCAAGTGACATCAGCTGGCTGTGATGCTTCGAAATAGGTCTGCTCCTCACAGC
TTTGGGAATCTGAATGGAAGAAGAAAAGAGAGAAGTTAACAACCTCCACTGGGGCAACTTTGTGAACATG
TAGGCACTTAGTCATAGGAAACATATTATGTGCAGGTCCTAGCCTGGGGTAGGAAAGTAGATAGACAGAA
AATCATTAGGTAATTTAAGTACTAAATTGGGCAGGGCTTTTTAGTATCAAATCACTACTAGACCGTTTAA
TTTGTTAAATTATCTCTAGGATGGTGATTTATAACCTACCCAAAGTTATCGATATTCTTACTAAACTCTG
AGGCCTGAAGTTCTGTGATAGACCTTAAATAAGTGTCCTAAGTCAGTGGTTCCCAAATCTGGCTGGTCGG
GAATACCTGGGAAGTTTGTTAAAATTTTTTAAAAATGTTTTAAGATTTTTGGGTCCTGAGCCAGGCGTGG

TGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGATCGCCTGAGGTCAGGAGTTCAA
GATCAACCTGGCCAACATACTGAAACCCCGTCTCTACTAAAAATAAGAAAAATTAGCTGGGCGTGGTGGC
GGGCACCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGTTAGAGGTT
GCAGTGAGCTGAGATCACACCATTGCGCTTCAGCCTGGGCAACAAGAGTGAAACTCCATCTCC

>gi|8923041|ref|NM_017633.1| Homo sapiens chromosome 6 open reading frame 37 (C6orf37), mRNA
ACAACTGCTAAAGCTCCAGAGACACGAGCGTGTGTGGCAGCAAGAGCCGCCAGTTCGGGACCACCGCAGC
TGGGGTGGCAGCGGCGCAGGAGGGGTCGCGGGGCGGGAGTGGTGAGCGCAGGCGGCAGGGGTCTGGGAAA
GACGAAGTCGCTATTTGCTGTCTGAGCGCGCTCGCAGCTCCTGGAAGTGTTGCCGCCTCTCGGTTTCGCT
CTCGCTCGCTGCGCTCCTAGAAGGGGCGGCCGCCTCCAGGACTGACCAGGGCCAAGTGGCGCTCGGCGGG
CACTACATGGCGGAGGGTGAAGGGTACTTCGCCATGTCTGAGGACGAGCTGGCCTGCAGCCCCTACATCC
CCCTAGGCGGCGACTTCGGCGGCGGCGACTTCGGCGGCGGCGACTTCGGCGGCGGCGACTTCGGCGGCGG
CGACTTCGGCGGTGGCGGCAGCTTCGGTGGGCATTGCTTGGACTATTGCGAAAGCCCTACGGCGCACTGC
AATGTGCTGAACTGGGAGCAAGTGCAGCGGCTGGACGGCATCCTGAGTGAGACCATTCCGATTCACGGGC
GCGGCAACTTCCCCACGCTCGAGCTGCAGCCGAGCCTGATCGTGAAGGTGGTGCGGCGGCGCCTGGCCGA
GAAGCGCATTGGCGTCCGCGACGTGCGCCTCAACGGCTCGGCAGCCAGCCATGTCCTGCACCAGGACAGC
GGCCTGGGCTACAAGGACCTGGACCTCATCTTCTGCGCCGACCTGCGCGGGGAAGGGGAGTTTCAGACTG
TGAAGGACGTCGTGCTGGACTGCCTGTTGGACTTCTTACCCGAGGGGGTGAACAAAGAGAAGATCACACC
ACTCACGCTCAAGGAAGCTTATGTGCAGAAAATGGTTAAAGTGTGCAATGACTCTGACCGATGGAGTCTT
ATATCCCTGTCAAACAACAGTGGCAAAAATGTGGAACTGAAATTTGTGGATTCCCTCCGGAGGCAGTTTG
AATTCAGTGTAGATTCTTTTCAAATCAAATTAGACTCTCTTCTGCTCTTTTATGAATGTTCAGAGAACCC
AATGACTGAGACATTTCACCCCACAATAATCGGGGAGAGCGTCTATGGCGATTTCCAGGAAGCCTTTGAT
CACCTTTGTAACAAGATCATTGCCACCAGGAACCCAGAGGAAATCCGAGGGGGAGGCCTGCTTAAGTACT
GCAACCTCTTGGTGAGGGGCTTTAGGCCCGCCTCTGATGAAATCAAGGCCCTTCAAAGGTACATGTGTTC
CAGGTTTTTCATCGACTTCTCAGACATTGGAGAGCAGCAGAGAAAACTGGAGTCCTATTTGCAGAACCAC
TTTGTGGGATTGGAAGACCGCAAGTATGAGTATCTCATGACCCTTCATGGAGTGGTAAATGAGAGCACAG
TGTGCCTGATGGGACATGAAAGAAGACAGACTTTAAACCTTATCACCATGCTGGCTATCCGGGTGTTAGC
TGACCAAAATGTCATTCCTAATGTGGCTAATGTCACTTGCTATTACCAGCCAGCCCCCTATGTAGCAGAT
GCCAACTTTAGCAATTACTACATTGCACAGGTTCAGCCAGTATTCACGTGCCAGCAACAGACCTACTCCA
CTTGGCTACCCTGCAATTAAGAATCATTTAAAAATGTCCTGTGGGGAAGCCATTTCAGACAAGACAGGAG
AGAAAAAAAAAAAAAAAAAAAA

>gi|8923191|ref|NM_017709.1| Homo sapiens hypothetical protein FLJ20202 (FLJ20202), mRNA
TCTCTCACTCGGTGCCGCTGCCTAGGGGCTGTAGAGGTCGCGCCGCTCCTGCTGGGGCCTGCCCACGCCA
AGGACCTGCCTCTGTCGCCTCCTCTTCTATTGCCCAGTTTCCCCAGCCAGAACATCCCCTGAAGATGGCA
GAGGAGAGCAGCTGTACCAGGGATTGCATGTCCTTCAGCGTGCTCAACTGGGATCAGGTTAGCCGGCTGC
ATGAGGTCCTCACTGAAGTTGTACCTATCCACGGACGAGGCAACTTTCCAACCTTGGAGATAACTCTGAA
GGACATCGTCCAGACCGTCCGCAGTCGGCTGGAGGAGGCAGGCATCAAAGTGCACGACGTCCGGCTGAAT
GGCTCCGCAGCTGGCCACGTTTTGGTCAAAGATAATGGCTTGGGCTGCAAAGACCTGGACCTAATCTTCC
ATGTGGCTCTTCCAACAGAGGCAGAATTTCAGCTGGTTAGAGATGTGGTTCTGTGTTCCCTTCTGAACTT
CCTGCCAGAGGGTGTGAACAAGCTCAAAATCAGTCCAGTCACTCTGAAGGAGGCATATGTGCAGAAGCTA
GTGAAGGTTTGCACGGACACTGTCCGCTGGAGCCTGATCTCCCTCTCCAACAAGAACGGGAAGAACGTGG
AGCTGAAGTTTGTCGACTCCATTCGGCGTCAGTTTGAGTTCAGTGTGGACTCTTTCCAAATCATCCTGGA
TTCTTTGCTTTTCTTCTATGACTGTTCCAATAATCCCATCTCTGAGCACTTCCACCCCACCGTGATTGGG
GAGAGCATGTACGGGGACTTTGAGGAAGCTTTTGACCATCTGCAGAACAGACTGATCGCCACCAAGAACC
CAGAAGAAATCAGAGGCGGGGGACTTCTCAAGTACAGCAACCTTCTTGTGCGGGACTTCAGGCCCACAGA
CCAGGAAGAAATCAAAACTCTAGAGCGCTACATGTGCTCCAGGTTCTTCATCGACTTCCCGGACATCCTT
GAACAGCAGAGGAAGTTGGAGACTTACCTTCAAAACCACTTCGCTGAAGAAGAGAGAAGCAAGTACGACT
ACCTCATGATCCTTCGCAGGGTGGTGAACGAGAGCACCGTGTGTCTCATGGGGCATGAACGCAGGCAGAC
TCTGAACCTCATCTCCCTCCTGGCCTTGCGTGTGCTGGCGGAACAAAACATCATCCCCAGTGCCACCAAC
GTCACCTGTTACTACCAGCCGGCCCCTTACGTCAGTGATGGCAACTTCAGCAACTACTACGTTGCCCATC
CTCCAGTCACCTACAGCCAGCCTTACCCTACCTGGCTGCCCTGTAACTAACCTTGAGACCTGAGGGTTTC
CACAGTGGGAACCCCAATAGGGCTAGGGCTCTCAGGTAGGGGAGCCTCCTTCTAGATGTAGGCATTTGGC
TTTTAAAGGGGAACTCAGCTCTGATTCTGCTTTTTTTTTTTTTTTTCCTTTGTGTACCCATTGGAATGGG
TCTACAGTGTATCATGAGCCAACCCTCAAAGGACCCGTATTACAGTGCCACGTTGGAAAACGCTACAGGA

AGCATGACCTATCCACATCTTTCCAAGATAGACACTAACATGTCATGTCCCAAACATTAGCACGTGGGGG
TTGAGCTCTGTGCAGTAATCGAGATTGGGAGAATTTGGGCAGCGCGTGAGAAGTGCTAAGCTACTTGTTT
TCTCACTTGAGCCCGGGTAGGCTGTGTTGGCCCTCACTTGGGATTCTCAGCAGTTACATGAAAGTTGTGC
TGATAATCTCTTCTCTTGTACCAATTTTAGTCAGGCAGAAAATGGTAAACATGAGGGTGCTCTTGTGACT
TAATTTTTGTTCAAGGGACTAAATTGCTTATGTTTATTCCCTGTCAGCGGAGTGGAGAATGTCATTCATC
AATAAACCAAAGCCAATAGCTGGAGAATTGAGATCTGGTTGAAAGTGGTTTATGGTTTACATGCTGTACT
ATCCTGAGGAATTGCGAGATATTGCTGAGGGGAAAAAAAAATGACCTTTTCTTGAAATGTAACTTGAAAA
CAAAATAAAATGTGGAACATAAAAAAAAAAAAAAAAAAAAAAAAAA

>gi|16418426|ref|NM_052943.1| Homo sapiens hypothetical protein MGC16491 (MGC16491), mRNA
GGCACGAGGGTTAGTCGTCGCCGTCTGAGGTGTTCCCTGGCTTTGTCTCGCCGTCGTTGCCGCCCCGTCC
CTGCCTTCGTGCCCCCCGCCTTGGCCCCTGCCCAGCCGCTCTCCCTGTCCTCCTCCCCTTAACCACCCCC
ACGGTTTCTGCCGTCGGGGCCCGGGGGCCGGGCGGATGATGCCGTCGGAGAGCGGAGCTGAGCGCAGGGA
CCGGGCGGCTGCTCAGGTGGGGACGGCTGCGGCCACGGCGGTGGCCACGGCAGCCCCGGCAGGCGGCGGC
CCCGACCCGGAGGCCTTATCGGCCTTCCCCGGACGGCACCTGAGTGGGCTGAGCTGGCCACAGGTGAAGC
GACTGGACGCTCTTCTGAGCGAGCCGATTCCCATTCACGGGCGCGGCAACTTCCCCACGCTGAGCGTGCA
GCCCCGGCAGATCGTGCAGGTGGTCCGCAGCACCCTGGAGGAGCAGGGACTACATGTGCACAGTGTGCGG
CTGCATGGTTCAGCTGCCAGCCACGTGCTGCACCCTGAGAGTGGCCTGGGCTACAAGGATCTGGACCTGG
TGTTCCGGGTGGACCTGCGCAGTGAGGCATCCTTCCAGCTGACCAAGGCAGTGGTGCTGGCCTGCCTACT
AGACTTCCTGCCGGCCGGTGTGAGCCGGGCCAAGATCACGCCACTGACACTCAAGGAGGCATACGTGCAG
AAGCTGGTGAAAGTGTGCACAGACTCGGACCGCTGGAGCCTCATCTCACTGTCCAACAAGAGCGGCAAGA
ACGTGGAGCTCAAGTTTGTGGACTCGGTGAGACGCCAGTTTGAATTCAGCATAGACTCCTTCCAGATCAT
CCTGGACTCCCTGTTGCTCTTTGGCCAGTGCTCGTCCACTCCCATGTCTGAGGCCTTCCACCCAACGGTC
ACAGGCGAAAGCCTGTACGGGGACTTCACCGAGGCCCTGGAGCACCTGCGGCACCGTGTCATCGCCACGC
GCAGTCCCGAGGAGATCCGAGGTGGTGGCCTCCTCAAGTACTGCCACCTCCTGGTGCGGGGCTTCCGGCC
CCGGCCCAGCACCGATGTGCGCGCCCTGCAGCGCTACATGTGCTCCCGCTTCTTCATCGACTTTCCAGAC
CTGGTGGAGCAGCGGCGCACCCTAGAGCGCTACCTGGAGGCCCACTTCGGTGGGGCAGATGCAGCCCGCC
GTTACGCCTGCCTGGTGACACTGCACCGGGTGGTCAACGAGAGCACCGTGTGCCTCATGAACCACGAGCG
CCGCCAGACGCTGGACCTCATTGCCGCACTGGCGCTGCAGGCACTGGCTGAGCAGGGCCCAGCTGCCACT
GCCGCCCTGGCCTGGCGCCCTCCAGGCACTGACGGGGTTGTGCCAGCCACTGTCAATTACTACGTGACCC
CCGTGCAACCTCTCCTGGCTCACGCCTATCCCACCTGGCTGCCTTGTAACTGACTCAGACCCTGGCCAGA
AGGGAAGGGACTGGGCCTCACGGGGTGGGGTGGGGCCTCCAAGAGTGTGTGGAGGACATGACCAGAGGCG
CAGAATGTGCCAGGAGGCCCAGCACTGCAGGGTTGGGCCTTTGATTGAACAGACCAGACTTTCCCGAGCA
CGAGGCCCCTGTGGGCTTAATGCCAGCCTGGGGCTCTCAGCAGGAGGACCCTTTGGTTATTGCATCACAC
TTTTGGACCAGCATGCCGGTGGGGTGCAGGCGCCATTTGTCTTGGAAGTCAATTTCCTTCAGGAGACAAA
GCAAGTTTGGGGTGGTAGCCTTAATGCCCAGCACCTTGGATTGATTCCCATGGTCTAAGAGGGTCTTTTT
GACTAAGGCCAGCCTGTGGTGATCCCAGCAGCTTTGGAGGGCCTGCAGCCCACACACTGACTGATACATG
GTATGTTACAGGGACTTGTCACTTTGGATCAGGCTGGGCCACTACAGGGCCTGATGGGCCAACTTGGGTA
ATCACTGGGAGGAGGGAAACTGAGGCCCGAGGCAGATACCTGGGTTTGGGGAGGGCTGGGTTTAGCCCGG
TTCTCTGAACTACATACCCCCAGCTGTGAAGCCTTCCTCTTGAGGGGTTGAGGTGGGCAGTATACAGGAG
CCAAGCAGCCCAGGGTGGGTCGCAGCCCAGGCCCCTTCCAGGGTGCCACTCCTTTCCCCCTTGTGTTGCA
AGGAGCCCTCCTGCCTGGGAGCTTGTTCTTTGGAAGGTGCTGAGCCTGAATTTGCCACAGTCAAGTCAAC
GTTCCCACCCCACTGGCTTGGTTACAGGGCTCTCACATGGGGTAGGGGAGCCATACTCCCACCCCCTTGC
GTATTCCCCTGGGTTTGTTGATATTTTGCACTCTTAACACCTGCCAATAAAGACGGTCTACACTGAAAAA
AAAAAAAAAAAAAA

>gi|22749286|ref|NM_152630.1| Homo sapiens hypothetical protein MGC26999 (MGC26999), mRNA
AGCGGGAATGTGTGGAGATCAGGTGATGCAGAACTCTGGTAAAGGATGTTAGTCTTCAGAGTAAGACTGT
TAAATTCAGCAAAGTCTACTATCAGAAGACACGTTTTTCTGGTTGGTGTATTACTTTATTCAGTGATAAT
ATGAAAATTACTATCTTCACTGAAGGATCTACTGAATAATCATTTTAACTCAACTATATTGCATTCTTGA
AAGCAATCCTTTCAATTGATCTACTGACTTCACAATGTCTGAAATCAGATTCACCAATCTCACTTGGGAT
CAAGTTATAACACTGGATCAAGTGTTAGATGAAGTAATTCCAATTCATGGAAAGGGGAATTTCCCCACAA
TGGAGGTAAAACCAAAAGACATCATTCATGTTGTGAAAGATCAACTCATAGGGCAAGGAATTATTGTTAA
AGATGCCAGATTGAATGGTTCCGTAGCAAGTTACATACTTGCAAGCCACAATGGAATCAGCTATAAGGAT
CTGGACGTTATTTTTGGTGTTGAGCTTCCAGGTAACGAAGAATTTCAGGTTGTTAAAGATGCAGTTCTAG

ACTGTCTACTTGACTTTTTACCAAAAGATGTAAAGAAGGAAAAGCTCTCCCCAGATATCATGAAAGACGC
TTACGTACAGAAATTGGTCAAGGTTTGCAATGGGCATGATTGTTGGAGTCTTATCTCCCTTTCAAATAAC
ACTGGGAAGAATTTAGAACTAAAATTTGTGAGTTCACTCAGACGGCAGTTTGAATTTAGTGTAGATTCCT
TTCAAATTGTTTTGGATCCCATGTTAGACTTCTACAGTGACAAAAATGCCAAGCTAACCAAAGAATCCTA
TCCTGTTGTGGTAGCTGAAAGCATGTATGGAGACTTCCAGGAAGCAATGACACATTTGCAACACAAGCTC
ATATGTACCAGGAAACCTGAAGAGATTAGAGGTGGTGGCCTTCTGAAGTACTGCAGCTTGCTGGTTCATG
GCTTCAAGCCAGCCTGTATGTCAGAAATCAAAAACCTAGAACGTTATATGTGCTCTAGATTCTTTATTGA
TTTTCCTCATATAGAAGAACAGCAAAAGAAAATTGAATCATACCTCCACAACCATTTCATAGGTGAAGGA
ATGACCAAGTATGACTACCTTATGACCTTGCATGGAGTTGTGAATGAAAGCACTGTTTGCCTCATGAGTT
ATGAAAGAAGACAGATTCTCCACCTGATCACCATGATGGCTTTGAAAGTACTTGGAGAACTAAATATTCT
ACCCAATACACAAAAGGTAACTTGCTTTTATCAGCCTGCTCCGTACTTTGCAGCTGAGGCAAGGTACCCT
ATTTATGTAATACCTGAGCCACCCCCCGTTAGCTTCCAGCCATACCACCCACTGCACTTTCGTGGATCAA
ATGGTATGAGTTAAAAAATACACATGCAACCATAGAAACTTTGATTTAATTAAACACCATTTAAAAGCAA
GTTTCCAAATGTAAAATTCAAGATCTGTTTTTATTTTTGTACAGTTACCAATTATTTTCAATTACAGTTG
ATGGAATAGTAGTTACCAACTATTTTTGATCAATTAAGCCATCATAGTAAATACAATATCTATAAACCAA
CCACTTTAAATGTTTTTCAAACGTTATTGACTAGCTATAATAACTTTCAAATGTTGTGTTCCCCTTGAAG
TGATTTTCAAATCTTTTGACTACTTGTGACTTTCAAATTTACTGTGACAAATATATTAGAGATGCCTGCA
TCTTTGACTATAACATAAAAGGACAGATTCATGTTTTAAAATTAAGATGTACAGTGAAGTATCAAATTTT
TTATATTCAGTCAGTTCCTTTGTTACATTTAGTTCTTTTTTTCTATTGAACAATACCATCAATAAATGTT
CAGTACTTAACAGAAATGCCTAATTTCAAAAGCAACAGATTCAGAAGACATTAAAACCCTGGACTTTTCA
AGCATTTTTTTTTGACAATTAAATTGGGTTGGATACAAAAATCCTACTATAGTTTAAAGGAATACTGGAA
AAAAATGGTTCTGGAAAGCCCTGGACATTAGTAATTTGTCATCTATATAATAAAACATTTAGTTAATTTG
TGGATTTGAATAACAATACCATACAGCTGTGCAACTACTACTGAGATCAGATACAGGGTTTTTTGCCCCT
CAAAATAAGTTAAAACGAATGAAAATGACCAGCTCTGAATGTGAAAGCTTTCTATCATCATCTACTACAA
AGAGACTCTAAATGGCAAACAGGAAAAAAACAGGCAGAGGTTTATAGCCATAGCATTTACCATTTTATGG
CTTATTTGAAAAACATCTTTATGTTGAGAAACATTCCATTTCAGTAAGTTAAAATATTTTCATTGTAACT
AAATGAAGCAGGTTTTTCATTTTGCCTTTACCAAAGATCATTTTCTAACATGCCACTCAAGTGCCTCTTC
GTGTGAATTTTTGCGTAACACTATAATTTATTCAACAACTGTATACCTTTACAGTATATCTAAATATATA
CTTACTACATCGAGTATACTGCTAGAAAAATCTACCAGTGGGATTAAAAATGTATTTTCTTCCCATAATG
AAAATAATTCATGACCAATATTACCTGAAGTGTCAGAAGAGGAGCTGTCTTAAATTAATATGGATCAGGC
CATTGGAAAACTTCAGTATTTCCACTTGGTTATGATTTTTTGTGAGTTTCCATTTCAGTTTTTATTGACC
ATCACGTTTTCTATCACAACATGACCTGACAGTTGTATCCCGATAATTTGCCAGTTATAGACTGTGCTTA
TCTTCACTGTATTACAATATTGGACAGAAGTACACCAAATACGGCATTTTCAAATAACCAATATTTCTGA
GATGTTTTATACCACAGCACAAGTGGCCATCAGTATATTTTTAAAGAATTATATATCACAGAACCCTGAG
GCTTTAAAACACTATGGACTTACCACTTTCTTGACAAAGAATTTGTAATTACAATAAAATATTTAGAAAT
GAAAGGCAAAAAAAAAAAAAAAA

>gi|22212711|gb|AAM94374.1|AF497517_1 adenylate cyclase type V [Homo sapiens]
TNAQDQFLLKQLVSNVLIFSCTNIVGVCTHYPAEVSQRQAFQETRECIQARLHSQRENQQQERLLLSVLP
RHVAMEMKADINAKQEDMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAE
NHCLRIKILGDCYYCVSGLPEARADHAHCCVEMGMDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGL
RKWQFDVWSNDVTLANHMEAGGKAGRIHITKATLNYLNGDYEVEPGCGGERNAYLKEHSIETFLILRCTQ
KRKEEKAMIAKMNRQRTNSIGHNPPHWGAERPFYNHLGGNQVSKEMKRMGFEDPKDKNAQESANPEDEVD
EFLGRAIDARSIDRLRSEHVRKFLLTFREPDLEKKYSKQVDDRFGAYVACASLVFLFICFVQITIVPHSI
FMLSFYLTCSLLLTLVVFVSVIYSCVKLFPSPLQTLSRKIVRSKMNSTLVGVFTITLVFLAAFVNMFTCN
SRDLLGCLAQEHNISASQVNACHVAESAVNYSLGDEQGFCGSPWPNCNFPEYFTYSVLLSLLACSVFLQI
SCIGKLVLMLAIELIYVLIVEVPGVTLFDNADLLVTANAIDFFNNGTSQCPEHATKVALKVVTPIIISVF
VLALYLHAQQVESTARLDFLWKLQATEEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYYQSC
ECVAVMFASIANFSEFYVELEANNEGVECLRLLNEIIADFDEIISEDRFRQLEKIKTIGSTYMAASGLND
STYDKVGKTHIKALADFAMKLMDQMKYINEHSFNNFQMKIGLNIGPVVAGVIGARKPQYDIWGNTVNVAS
RMDSTGVPDRIQVTTDMYQVLAANTYQLECRGVVKVKGKGEMMTYFLNGGPPLS

>gi|10181096|ref|NP_056085.1| adenylate cyclase 6 isoform a [Homo sapiens]
MSWFSGLLVPKVDERKTAWGERNGQKRSRRRGTRAGGFCTPRYMSCLRDAEPPSPTPAGPPRCPWQDDAF

IRRGGPGKGKELGLRAVALGFEDTEVTTTAGGTAEVAPDAVPRSGRSCWRRLVQVFQSKQFRSAKLERLY
QRYFFQMNQSSLTLLMAVLVLLTAVLLAFHAAPARPQPAYVALLACAAALFVGLMVVCNRHSFRQDSMWV
VSYVVLGILAAVQVGGALAADPRSPSAGLWCPVFFVYIAYTLLPIRMRAAVLSGLGLSTLHLILAWQLNR
GDAFLWKQLGANVLLFLCTNVIGICTHYPAEVSQRQAFQETRGYIQARLHLQHENRQQERLLLSVLPQHV
AMEMKEDINTKKEDMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAENHC
LRIKILGDCYYCVSGLPEARADHAHCCVEMGVDMIEAISLVREVTGVNVNMRVGIHSGRVHCGVLGLRKW
QFDVWSNDVTLANHMEAGGRAGRIHITRATLQYLNGDYEVEPGRGGERNAYLKEQHIETFLILGASQKRK
EEKAMLAKLQRTRANSMEGLMPRWVPDRAFSRTKDSKAFRQMGIDDSSKDNRGTQDALNPEDEVDEFLSR
AIDARSIDQLRKDHVRRFLLTFQREDLEKKYSRKVDPRFGAYVACALLVFCFICFIQLLIFPHSTLMLGI
YASIFLLLLITVLICAVYSCGSLFPKALQRLSRSIVRSRAHSTAVGIFSVLLVFTSAIANMFTCNHTPIR
SCAARMLNLTPADITACHLQQLNYSLGLDAPLCEGTMPTCSFPEYFIGNMLLSLLASSVFLHISSIGKLA
MIFVLGLIYLVLLLLGPPATIFDNYDLLLGVHGLASSNETFDGLDCPAAGRVALKYMTPVILLVFALALY
LHAQQVESTARLDFLWKLQATGEKEEMEELQAYNRRLLHNILPKDVAAHFLARERRNDELYYQSCECVAV
MFASIANFSEFYVELEANNEGVECLRLLNEIIADFDEIISEERFRQLEKIKTIGSTYMAASGLNASTYDQ
VGRSHITALADYAMRLMEQMKHINEHSFNNFQMKIGLNMGPVVAGVIGARKPQYDIWGNTVNVSSRMDST
GVPDRIQVTTDLYQVLAAKGYQLECRGVVKVKGKGEMTTYFLNGGPSS

>gi|4557257|ref|NP_001106.1| adenylate cyclase 8; Adenylyl cyclase-8, brain [Homo sapiens]

MELSDVRCLTGSEELYTIHPTPPAGDGRSASRPQRLLWQTAVRHITEQRFIHGHRGGSGSGSGGSGKASD
PAGGGPNHHAPQLSGDSALPLYSLGPGERAHSTCGTKVFPERSGSGSASGSGGGGDLGFLHLDCAPSNSD
FFLNGGYSYRGVIFPTLRNSFKSRDLERLYQRYFLGQRRKSEVVMNVLDVLTKLTLLVLHLSLASAPMDP
LKGILLGFFTGIEVVICALVVVRKDTTSHTYLQYSGVVTWVAMTTQILAAGLGYGLLGDGIGYVLFTLFA
TYSMLPLPLTWAILAGLGTSLLQVILQVVIPRLAVISINQVVAQAVLFMCMNTAGIFISYLSDRAQRQAF
LETRRCVEARLRLETENQRQERLVLSVLPRFVVLEMINDMTNVEDEHLQHQFHRIYIHRYENVSILFADV
KGFTNLSTTLSAQELVRMLNELFARFDRLAHEHHCLRIKILGDCYYCVSGLPEPRQDHAHCCVEMGLSMI
KTIRYVRSRTKHDVDMRIGIHSGSVLCGVLGLRKWQFDVWSWDVDIANKLESGGIPGRIHISKATLDCLN
GDYNVEEGHGKERNEFLRKHNIETYLIKQPEDSLLSLPEDIVKESVSSSDRRNSGATFTEGSWSPELPFD
NIVGKQNTLAALTRNSINLLPNHLAQALHVQSGPEEINKRIEHTIDLRSGDKLRREHIKPFSLMFKDSSL
EHKYSQMRDEVFKSNLVCAFIVLLFITAIQSLLPSSRVMPMTIQFSILIMLHSALVLITTAEDYKCLPLI
LRKTCCWINETYLARNVIIFASILINFLGAILNILWCDFDKSIPLKNLTFNSSAVFTDICSYPEYFVFTG
VLAMVTCAVFLRLNSVLKLAVLLIMIAIYALLTETVYAGLFLRYDNLNHSGEDFLGTKEVSLLLMAMFLL
AVFYHGQQLEYTARLDFLWRVQAKEEINEMKELREHNENMLRNILPSHVARHFLEKDRDNEELYSQSYDA
VGVMFASIPGFADFYSQTEMNNQGVECLRLLNEIIADFDELLGEDRFQDIEKIKTIGSTYMAVSGLSPEK
QQCEDKWGHLCALADFSLALTESIQEINKHSFNNFELRIGISHGSVVAGVIGAKKPQYDIWGKTVNLASR
MDSTGVSGRIQVPEETYLILKDQGFAFDYRGEIYVKGISEQEGKIKTYFLLGRVQPNPFILPPRRLPGQY
SLAAVVLGLVQSLNRQRQKQLLNENNNTGIIKGHYNRRTLLSPSGTEPGAQAEGTDKSDLP

>gi|7661962|ref|NP_055585.1| centaurin, gamma 1; centaurin gamma1; phosphoinositide 3-kinase enhancer; Arf GAP with GTP-binding protein-like, ANK repeat and PH domains 2; GTP-binding and GTPase activating protein 2 [Homo sapiens]

MHAQRQFVVAAVRAEVRRHEVAKQALNRLRKLAERVDDPELQDSIQASLDSIREAVINSQEWTLSRSIPE
LRLGVLGDARSGKSSLIHRFLTGSYQVLEKTESEQYKKEMLVDGQTHLVLIREEAGAPDAKFSGWADAVI
FVFSLEDENSFQAVSRLHGQLSSLRGEGRGGLALALVGTQDRISASSPRVVGDARARALCADMKRCSYYE
TCATYGLNVDRVFQEVAQKVVTLRKQQQLLAACKSLPSSPSHSAASTPVAGQASNGGHTSDYSSSLPSSP
NVGHRELRAEAAAVAGLSTPGSLHRAAKRRTSLFANRRGSDSEKRSLDSRGETTGSGRAIPIKQSFLLKR
SGNSLNKEWKKKYVTLSSNGFLLYHPSINDYIHSTHGKEMDLLRTTVKVPGKRPPRAISAFGPSASINGL
VKDMSTVQMGEGLEATTPMPSPSPSPSSLQPPPDQTSKHLLKPDRNLARALSTDCTPSGDLSPLSREPPP
SPMVKKQRRKKLTTPSKTEGSAGQAEEENFEFLIVSSTGQTWHFEAASFEERDAWVQAIESQILASLQCC
ESSKVKLRTDSQSEAVAIQAIRNAKGNSICVDCGAPNPTWASLNLGALICIECSGIHRNLGTHLSRVRSL
DLDDWPRELTLVLTAIGNDTANRVWESDTRGRAKPSRDSSREERESWIRAKYEQLLFLAPLSTSEEPLGR
QLWAAVQAQDVATVLLLLAHARHGPLDTSVEDPQLRSPLHLAAELAHVVITQLLLWYGADVAARDAQGRT
ALFYARQAGSQLCADILLQHGCPGEGGSAATTPSAATTPSITATPSPRRRSSAASVGRADAPVALV

>gi|7662484|ref|NP_055729.1| centaurin, gamma 2; Arf GAP with GTP-binding protein-like, ANK repeat and PH domains 1; GTP-binding and GTPase-activating protein 1 [Homo sapiens]
MNYQQQLANSAAIRAEIQRFESVHPNIYSIYELLERVEEPVLQNQIREHVIAIEDAFVNSQEWTLSRSVP
ELKVGIVGNLASGKSALVHRYLTGTYVQEESPEGGRFKKEIVVDGQSYLLLIRDEGGPPEAQFAMWVDAV
IFVFSLEDEISFQTVYHYYSRMANYRNTSEIPLVLVGTQDAISSANPRVIDDARARKLSNDLKRCTYYET
CATYGLNVERVFQDVAQKIVATRKKQQLSIGPCKSLPNSPSHSSVCSAQVSAVHISQTSNGGGSLSDYSS
SVPSTPSISQKELRIDVPPTANTPTPVRKQSKRRSNLFTSRKGSDPDKEKKGLESRADSIGSGRAIPIKQ
GMLLKRSGKSLNKEWKKKYVTLCDNGVLTYHPSLHDYMQNVHGKEIDLLRTTVKVPGKRPPRATSACAPI
SSPKTNGLSKDMSSLHISPNSDTGLGDSVCSSPSISSTTSPKLDPPPSPHANRKKHRRKKSTSNFKADGL
SGTAEEQEENFEFIIVSLTGQTWHFEATTYEERDAWVQAIESQILASLQSCESSKNKSRLTSQSEAMALQ
SIRNMRGNSHCVDCETQNPNWASLNLGALMCIECSGIHRNLGTHLSRVRSLDLDDWPIELIKVMSSIGNE
LANSVWEESSQGRTKPSVDSTREEKERWIRAKYEQKLFLAPLPCTELSLGQHLLRATADEDLRTAILLLA
HGSRDEVNETCGEGDGRTALHLACRKGNVVLAQLLIWYGVDVTARDAHGNTALAYARQASSQECIDVLLQ
YGCPDERFVLMATPNLSRRNNNRNNSSGRVPTII

>gi|16799069|ref|NP_114152.2| centaurin, gamma 3; MRIP-1 protein [Homo sapiens]
MNFQAGGGQSPQQQQQLAGGPPQQFALSNSAAIRAEIQRFESVHPNIYAIYDLIERIEDLALQNQIREHV
ISIEDSFVNSQEWTLSRSVPELKVGIVGNLSSGKSALVHRYLTGTYVQEESPEGGRFKKEIVVDGQSYLL
LIRDEGGPPELQFAAWVDAVVFVFSLEDEISFQTVYNYFLRLCSFRNASEVPMVLVGTQDAISAANPRVI
DDSRARKLSTDLKRCTYYETCATYGLNVERVFQDVAQKVVALRKKQQLAIGPCKSLPNSPSHSAVSAASI
PAVHINQATNGGGSAFSDYSSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTSRKGADLDRE
KKAAECKVDSIGSGRAIPIKQGILLKRSGKSLNKEWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLL
RTTVKVPGKRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSASLHSERPLSSSAWAGPRPE
GLHQRSCSVSSADQWSEATTSLPPGMQHPASGPAEVLSSSPKLDPPPSPHSNRKKHRRKKSTGTPRPDGP
SSATEEAEESFEFVVVSLTGQTWHFEASTAEERELWVQSVQAQILASLQGCRSAKDKTRLGNQNAALAVQ
AVRTVRGNSFCIDCDAPNPDWASLNLGALMCIECSGIHRHLGAHLSRVRSLDLDDWPPELLAVMTAMGNA
LANSVWEGALGGYSKPGPDACREEKERWIRAKYEQKLFLAPLPSSDVPLGQQLLRAVVEDDLRLLVMLLA
HGSKEEVNETYGDGDGRTALHLSSAMANVVFTQLLIWYGVDVRSRDARGLTPLAYARRAGSQECADILIQ
HGCPGEGCGLAPTPNREPANGTNPSAELHRSPSLL

>gi|5453840|ref|NP_006377.1| DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 isoform 1; probable RNA-dependent helicase p72 [Homo sapiens]
MRGGGFGDRDRDRDRGGFGARGGGGLPPKKFGNPGERLRKKKWDLSELPKFEKNFYVEHPEVARLTPYEV
DELRRKKEITVRGGDVCPKPVFAFHHANFPQYVMDVLMDQHFTEPTPIQCQGFPLALSGRDMVGIAQTGS
GKTLAYLLPAIVHINHQPYLERGDGPICLVLAPTRELAQQVQQVADDYGKCSRLKSTCIYGGAPKGPQIR
DLERGVEICIATPGRLIDFLESGKTNLRRCTYLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSATW
PKEVRQLAEDFLRDYTQINVGNLELSANHNILQIVDVCMESEKDHKLIQLMEEIMAEKENKTIIFVETKR
RCDDLTRRMRRDGWPAMCIHGDKSQPERDWVLNEFRSGKAPILIATDVASRGLDVEDVKFVINYDYPNSS
EDYVHRIGRTARSTNKGTAYTFFTPGNLKQARELIKVLEEANQAINPKLMQLVDHRGGGGGGGGRSRYRT
TSSANNPNLMYQDECDRRLRGVKDGGRRDSASYRDRSETDRAGYANGSGYGSPNSAFGAQAGQYTYGQGT
YGAAAYGTSSYTAQEYGAGTYGASSTTSTGRSSQSSSQQFSGIGRSGQQPQPLMSQQFAQPPGATNMIGY
MGQTAYQYPPPPPPPPPSRK

>gi|4758138|ref|NP_004387.1| DEAD (Asp-Glu-Ala-Asp) box polypeptide 5; DEAD box-5 [Homo sapiens]
MSGYSSDRDRGRDRGFGAPRFGGSRAGPLSGKKFGNPGEKLVKKKWNLDELPKFEKNFYQEHPDLARRTA
QEVETYRRSKEITVRGHNCPKPVLNFYEANFPANVMDVIARQNFTEPTAIQAQGWPVALSGLDMVGVAQT
GSGKTLSYLLPAIVHINHQPFLERGDGPICLVLAPTRELAQQVQQVAAEYCRACRLKSTCIYGGAPKGPQ
IRDLERGVEICIATPGRLIDFLECGKTNLRRTTYLVLDEADRMLDMGFEPQIRKIVDQIRPDRQTLMWSA
TWPKEVRQLAEDFLKDYIHINIGALELSANHNILQIVDVCHDVEKDEKLIRLMEEIMSEKENKTIVFVET
KRRCDELTRKMRRDGWPAMGIHGDKSQQERDWVLNEFKHGKAPILIATDVASRGLDVEDVKFVINYDYPN
SSEDYIHRIGRTARSTKTGTAYTFFTPNNIKQVSDLISVLREANQAINPKLLQLVEDRGSGRSRGRGGMK
DDRRDRYSAGKRGGFNTFRDRENYDRGYSSLLKRDFGAKTQNGVYSAANYTNGSFGSNFVSAGIQTSFRT
GNPTGTYQNGYDSTQQYGSNVPNMHNGMNQQAYAYPATAAAPMIGYPMPTGYSQ

>gi|8922581|ref|NP_060643.1| hypothetical protein FLJ10665 [Homo sapiens]
MKAFGPPHEGPLQGLVASRIETYGGRHRASAQSTTGRLYPRGYPVLDPSRRRLQQYVPFARGSGQARGLS
PMRLRDPEPEKRHGGHVGAGLLHSPKLKELTKAHELEVRLHTFSMFGMPRLPPEDRRHWEIGEGGDSGLT
IEKSWRELVPGHKEMSQELCHQQEALWELLTTELIYVRKLKIMTDLLAAGLLNLQRVGLLMEVSAETLFG
NVPSLIRTHRSFWDEVLGPTLEETRASGQPLDPIGLQSGFLTFGQRFHPYVQYCLRVKQTMAYAREQQET
NPLFHAFVQWCEKHKRSGRQMLCDLLIKPHQRITKYPLLLHAVLKRSPEARAQEALNAMIEAVESFLRHI
NGQVRQGEEQESLAAAAQRIGPYEVLEPPSDEVEKNLRPFSTLDLTSPMLGVASEHTRQLLLEGPVRVKE
GREGKLDVYLFLFSDVLLVTKPQRKADKAKVIRPPLMLDKLVCQPLRDPNSFLLIHLTEFQCVSSALLVH
CPSPTDRAQWLEKTQQAQAALQKLKAEEYVQQKRELLTLYRDQDRESPSTRPSTPSLEGSQSSAEGRTPE
FSTIIPHLVVTEDTDEDAPLVPDDTSDSGYGTLIPGTPTGSRSPLSRLRQRALRRDPRLTFSTLELRDIP
LRPHPPDPQAPQRRSAPELPEGILKGGSLPQEDPPTWSEEEDGASERGNVVVETLHRARLRGQLPSSPTH
ADSAGESPWESSGEEEEEGPLFLKAGHTSLRPMRAEDMLREIREELASQRIEGAEEPRDSRPRKLTRAQL
QRMRGPHIIQLDTPLSASEV

>gi|29728516|ref|XP_030970.8| similar to hypothetical protein FLJ10665 [Homo sapiens]
MNSVLTKHGSPPRSWLSLCSGTDDQSPAEKKGLRCQNPACMDKGRAAKVCHHADCQQLHRRGPLNLCEAC
DSKFHSTMHYDGHVRFDLPPQGSVLARNVSTRSCPPRTSPAVDLEEEEEESSVDGKGDRKSTGLKLSKKK
ARRRHTDDPSKECFTLKFDLNVDIETEIVPAMKKKSLGEVLLPVFERKGIALGKVDIYLDQSNTPLSLTF
EAYRFGGHYLRVKAPAKPGDEGKVEQGMKDSKSLSLPILRPAGTGPPALERVDAQSRRESLDILAPGRRR
KNMSEFLGEASIPGQEPPTPSSCSLPSGSSGSTNTGDSWKNRAASRFSGFFSSGPSTSAFGREVDKMEQL
EGKLHTYSLFGLPRLPRGLRFDHDSWEEEYDEDEDEDNACLRLEDSWRELIDGHEKLTRRQCHQQEAVWE
LLHTEASYIRKLRVIINLFLCCLLNLQESGLLCEVEAERLFSNIPEIAQLHRRLWASVMAPVLEKARRTR
ALLQPGDFLKGFKMFGSLFKPYIRYCMEEEGCMEYMRGLLRDNDLFRAYITWAEKHPQCQRLKLSDMLAK
PHQRLTKYPLLLKSVLRKTEEPRAKEAVVAMIGSVERFIHHVNACMRQRQERQRLAAVVSRIDAYEVVES
SSDEVDKLLKEFLHLDLTAPIPGASPEETRQLLLEGSLRMKEGKDSKMDVYCFLFTDLLLVTKAVKKAER
TRVIRPPLLVDKIVCRELRDPGSFLLIYLNEFHSAVGAYTFQASGQALCRGWVDTIYNAQNQLQQLRAQE
PPGSQQPLQSLEEEEDEQEEEEEEEEEEEEGEDSGTSAASSPTIMRKSSGSPDSQHCASDGSTETLAMVV
VEPGDTLSSPEFDSGPFSSQSDETSLSTTASSATPTSELLPLGPVDGRSCSMDSAYGTLSPTSLQDFVAP
GPMAELVPRAPESPRVPSPPPSPRLRRRTPVQLLSCPPHLLKSKSEASLLQLLAGAGTHGTPSAPSRSLS
ELCLAVPAPGIRTQGSPQEAGPSWDCRGAPSPGSGPGLVGCLAGEPAGSHRKRCGDLPSGASPRVQPEPP
PGVSAQHRKLTLAQLYRIRTTLLLNSTLTASEV

>gi|8923496|ref|NP_060334.1| hypothetical protein FLJ20530 [Homo sapiens]
MAAFLKNVCLGLEDLQYVFMISSHELFITLLKDEERKLLVDQMRKRSPRVNLCIKPVTSFYDIPASASVN
IGQLEHQLILSVDPWRIRQILIELHGMTSERQFWTVSNKWEVPSVYSGVILGIKDNLTRDLVYILMAKGL
HCSTVKDFSHAKQLFAACLELVTEFSPKLRQVMLNEMLLLDIHTHEAGTGQAGERPPSDLISRVRGYLEM
RLPDIPLRQVIAEECVAFMLNWRENEYLTLQVPAFLLQSNPYVKLGQLLAATCKELPGPKESRRTAKDLW
EVVVQICSVSSQHKRGNDGRVSLIKQRESTLGIMYRSELLSFIKKLREPLVLTIILSLFAKLHNVREDIV
NDITAEHISIWPSSIPNLQSVDFEAVAITVKELVRYTLSINPNNHSWLIIQADIYFATNQYSAALHYYLQ
AGAVCSDFFNKAVPPDVYTDQVIKRMIKCCSLLNCHTQVAILCQFLREIDYKTAFKSLQEQNSHDAMDSY
YDYIWDVTILEYLTYLHHKRGETDKRQIAIKAIGQTELNASNPEEVLQLAAQRRKKKFLQAMAKLYF

>gi|4557601|ref|NP_000798.1| gamma-aminobutyric acid A receptor, alpha 2 precursor [Homo sapiens]
MKTKLNIYNIEFLLFVFLVWDPARLVLANIQEDEAKNNITIFTRILDRLLDGYDNRLRPGLGDSITEVFT
NIYVTSFGPVSDTDMEYTIDVFFRQKWKDERLKFKGPMNILRLNNLMASKIWTPDTFFHNGKKSVAHNMT
MPNKLLRIQDDGTLLYTMRLTVQAECPMHLEDFPMDAHSCPLKFGSYAYTTSEVTYIWTYNASDSVQVAP
DGSRLNQYDLLGQSIGKETIKSSTGEYTVMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFWLNRESVP
ARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWTWDGKSVV
NDKKKEKASVMIQNNAYAVAVANYAPNLSKDPVLSTISKSATTPEPNKKPENKPAEAKKTFNSVSKIDRM
SRIVFPVLFGTFNLVYWATYLNREPVLGVSP

>gi|4503861|ref|NP_000801.1| gamma-aminobutyric acid (GABA) A receptor, alpha 5 precursor [Homo sapiens]

MDNGMFSGFIMIKNLLLFCISMNLSSHFGFSQMPTSSVKDETNDNITIFTRILDGLLDGYDNRLRPGLGE
RITQVRTDIYVTSFGPVSDTEMEYTIDVFFRQSWKDERLRFKGPMQRLPLNNLLASKIWTPDTFFHNGKK
SIAHNMTTPNKLLRLEDDGTLLYTMRLTISAECPMQLEDFPMDAHACPLKFGSYAYPNSEVVYVWTNGST
KSVVVAEDGSRLNQYHLMGQTVGTENISTSTGEYTIMTAHFHLKRKIGYFVIQTYLPCIMTVILSQVSFW
LNRESVPARTVFGVTTVLTMTTLSISARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGWA
WDGKKALEAAKIKKKREVILNKSTNAFTTGKMSHPPNIPKEQTPAGTSNTTSVSVKPSEEKTSESKKTYN
SISKIDKMSRIVFPVLFGTFNLVYWATYLNREPVIKGAASPK

>gi|4504019|ref|NP_000162.1| glycine receptor, alpha 1 [Homo sapiens]
MYSFNTLRLYLSGAIVFFSLAASKEAEAARSATKPMSPSDFLDKLMGRTSGYDARIRPNFKGPPVNVSCN
IFINSFGSIAETTMDYRVNIFLRQQWNDPRLAYNEYPDDSLDLDPSMLDSIWKPDLFFANEKGAHFHEIT
TDNKLLRISRNGNVLYSIRITLTLACPMDLKNFPMDVQTCIMQLESFGYTMNDLIFEWQEQGAVQVADGL
TLPQFILKEEKDLRYCTKHYNTGKFTCIEARFHLERQMGYYLIQMYIPSLLIVILSWISFWINMDAAPAR
VGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCLLFVFSALLEYAAVNFVSRQHKELLRFRRKRR
HHKEDEAGEGRFNFSAYGMGPACLQAKDGISVKGANNSNTTNPPPAPSKSPEEMRKLFIQRAKKIDKISR
IGFPMAFLIFNMFYWIIYKIVRREDVHNQ

>gi|20127457|ref|NP_004121.2| glycogenin [Homo sapiens]
MTDQAFVTLTTNDAYAKGALVLGSSLKQHRTTRRLVVLATPQVSDSMRKVLETVFDEVIMVDVLDSGDSA
HLTLMKRPELGVTLTKLHCWSLTQYSKCVFMDADTLVLANIDDLFDREELSAAPDPGWPDCFNSGVFVYQ
PSVETYNQLLHLASEQGSFDGGDQGILNTFFSSWATTDIRKHLPFIYNLSSISIYSYLPAFKVFGASAKV
VHFLGRVKPWNYTYDPKTKSVKSEAHDPNMTHPEFLILWWNIFTTNVLPLLQQFGLVKDTCSYVNVLSDL
VYTLAFSCGFCRKEDVSGAISHLSLGEIPAMAQPFVSSEERKERWEQGQADYMGADSFDNIKRKLDTYLQ

>gi|5453674|ref|NP_003909.1| glycogenin 2 [Homo sapiens]
MSETEFHHGAQAGLELLRSSNSPTSASQSAGMTVTDQAFVTLATNDIYCQGALVLGQSLRRHRLTRKLVV
LITPQVSSLLRVILSKVFDEVIEVNLIDSADYIHLAFLKRPELGLTLTKLHCWTLTHYSKCVFLDADTLV
LSNVDELFDRGEFSAAPDPGWPDCFNSGVFVFQPSLHTHKLLLQHAMEHGSFDGADQGLLNSFFRNWSTT
DIHKHLPFIYNLSSNTMYTYSPAFKQFGSSAKVVHFLGSMKPWNYKYNPQSGSVLEQGSVSSSQHQAAFL
HLWWTVYQNNVLPLYKSVQAGEARASPGHTLCHSDVGGPCADSASGVGEPCENSTPSAGVPCANSPLGSN
QPAQGLPEPTQIVDETLSLPEGRRSEDMIACPETETPAVITCDPLSQPSPQPADFTETETILQPANKVES
VSSEETFEPSQELPAEALRDPSLQDALEVDLAVSVSQISIEEKVKELSPEEERRKWEEGRIDYMGKDAFA
RIQEKLDRFLQ

>gi|30147855|ref|XP_301113.1| similar to Glycogenin-1 [Homo sapiens]
MTDQVFVTLTTNDAYTKGALVLGSSLKQHRTTRRLVMLATPQVSDSMRKVLETVFDEIIVVDVLDSGDSA
HLTLMKRPELAFKVFGASAKVVHFLGQVKPWNYTYDPKTKSVKNESHHPNVTHPEFLILWWNIFTTTVLP
LLQQFGLVKDTFSYVNVENVSGAISHLSLGGIPAMAQSVYPQKNGRSGGNRARPIIWEQIPLTTSRGSLT
LTSSRNTAFSCGHIHFTSLVSDT

>gi|4757726|ref|NP_004632.1| myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophil; ALL1 fused gene from chromosome 10; myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 [Homo sapiens]
MVSSDRPVSLEDEVSHSMKEMIGGCCVCSDERGWAENPLVYCDGHGCSVAVHQACYGIVQVPTGPWFCRK
CESQERAARVRCELCPHKDGALKRTDNGGWAHVVCALYIPEVQFANVSTMEPIVLQSVPHDRYNKTCYIC
DEQGRESKAATGACMTCNKHGCRQAFHVTCAQFAGLLCEEEGNGADNVQYCGYCKYHFSKLKKSKRGSNR
SYDQSLSDSSSHSQDKHHEKEKKKYKEKDKHKQKHKKQPEPSPALVPSLTVTTEKTYTSTSNNSISGSLK
RLEDTTARFTNANFQEVSAHTSSGKDVSETRGSEGKGKKSSAHSSGQRGRKPGGGRNPGTTVSAASPFPQ
GSFSGTPGSVKSSSGSSVQSPQDFLSFTDSDLRNDSYSHSQQSSATKDVHKGESGSQEGGVNSFSTLIGL
PSTSAVTSQPKSFENSPGDLGNSSLPTAGYKRAQTSGIEEETVKEKKRKGNKQSKHGPGRPKGNKNQENV
SHLSVSSASPTSSVASAAGSITSSSLQKSPTLLRNGSLQSLSVGSSPVGSEISMQYRHDGACPTTTFSEL
LNAIHNDRGDSSTLTKQELKFIGIYNSNDVAVSFPNVVSGSGSSTPVSSSHLPQQSSGHLQQVGALSPSA
VSSAAPAVATTQANTLSGSSLSQAPSHMYGNRSNSSMAALIAQSENNQTDQDLGDNSRNLVGRGSSPRGS
LSPRSPVSSLQIRYDQPGNSSLENLPPVAASIEQLLERQWSEGQQFLLEQGTPSDILGMLKSLHQLQVEN
RRLEEQIKNLTAKKERLQLLNAQLSVPFPTITANPSPSHQIHTFSAQTAPTTDSLNSSKSPHIGNSFLPD
NSLPVLNQDLTSSGQSTSSSSALSTPPPAGQSPAQQGSGVSGVQQVNGVTVGALASGMQPVTSTIPAVSA

VGGIIGALPGNQLAINGIVGALNGVMQTPVTMSQNPTPLTHTTVPPNATHPMPATLTNSASGLGLLSDQQ
RQILIHQQQFQQLLNSQQLTPVHRHPHFTQLPPTHFSPSMEIMQVRK

>gi|5174577|ref|NP_005928.1| myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6; Myeloid/lymphoid or mixed-lineage leukemia, translocated to, 6; myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 6 [Homo sapiens]
MKEMVGGCCVCSDERGWAENPLVYCDGHACSVAVHQACYGIVQVPTGPWFCRKCESQERAARVRCELCPH
KDGALKRTDNGGWAHVVCALYIPEVQFANVLTMEPIVLQYVPHDRFNKTCYICEETGRESKAASGACMTC
NRHGCRQAFHVTCAQMAGLLCEEEVLEVDNVKYCGYCKYHFSKMKTSRHSSGGGGGGAGGGGGSMGGGGS
GFISGRRSRSASPSTQQEKHPTHHERGQKKSRKDKERLKQKHKKRPESPPSILTPPVVPTADKVSSSASS
SSHHEASTQETSESSRESKGKKSSSHSLSHKGKKLSSGKGVSSFTSASSSSSSSSSSSGGPFQPAVSSLQ
SSPDFSAFPKLEQPEEDKYSKPTAPAPSAPPSPSAPEPPKADLFEQKVVFSGFGPIMRFSTTTSSSGRAR
APSPGDYKSPHVTGSGASAGTHKRMPALSATPVPADETPETGLKEKKHKASKRSRHGPGRPKGSRNKEGT
GGPAAPSLPSAQLAGFTATAASPFSGGSLVSSGLGGLSSRTFGPSGSLPSLSLESPLLGAGIYTSNKDPI
SHSGGMLRAVCSTPLSSSLLGPPGTSALPRLSRSPFTSTLPSSSASISTTQVFSLAGSTFSLPSTHIFGT
PMGAVNPLLSQAESSHTEPDLEDCSFRCRGTSPQESLSSMSPISSLPALFDQTASAPCGGGQLDPAAPGT
TNMEQLLEKQGDGEAGVNIVEMLKALHALQKENQRLQEQILSLTAKKERLQILNVQLSVPFPALPAALPA
ANGPVPGPYGLPPQAGSSDSLSTSKSPPGKSSLGLDNSLSTSSEDPHSGCPSRSSSSLSFHSTPPPLPLL
QQSPATLPLALPGAPAPLPPQPQNGLGRAPGAAGLGAMPMAEGLLGGLAGSGGLPLNGLLGGLNGAAAPN
PASLSQAGGAPTLQLPGCLNSLTEQQRHLLQQQEQQLQQLQQLLASPQLTPEHQTVVYQMIQQIQQKREL
QRLQMAGGSQLPMASLLAGSSTPLLSAGTPGLLPTASAPPLLPAGALVAPSLGNNTSLMAAAAAAAAVAA
AGGPPVLTAQTNPFLSLSGAEGSGGGPKGGTADKGASANQEKG

>gi|4505957|ref|NP_002688.1| POU domain, class 2, transcription factor 1; Octamer-binding transcription factor-1 [Homo sapiens]
MNNPSETSKPSMESGDGNTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSLQAAAQSLNV
QSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLAGGQITGLTLTPAQQQLLLQQAQAQAQLLAAAVQQH
SASQQHSAAGATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFVLVHPTTNLQPAQFIISQ
TPQGQQGLLQAQNLQTQLPQQSQANLLQSQPSITLTSQPATPTRTIAATPIQTLPQSQSTPKRIDTPSLE
EPSDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTISRFEALNLSFKNMCKLKPLLEKWL
NDAENLSSDSSLSSPSALNSPGIEGLSRRRKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEK
EVIRVWFCNRRQKEKRINPPSSGGTSSSPIKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVT
NLSVTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEASSASETSTTQTTSTPLSSPLGTS
QVMVTASGLQTAAAAALQGAAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLSGALSPAL
MSNSTLATIQALASGGSLPITSLDATGNLVFANAGGAPNIVTAPLFLNPQNLSLLTSNPVSLVSAAAASA
GNSAPVASLHATSTSAESIQNSLFTVASASGAASTTTTASKAQ

>gi|4505959|ref|NP_002689.1| POU domain, class 2, transcription factor 2 [Homo sapiens]
MVHSSMGAPEIRMSKPLEAEKQGLDSPSEHTDTERNGPDTNHQNPQNKTSPFSVSPTGPSTKIKAEDPSG
DSAPAAPLPPQPAQPHLPQAQLMLTGSQLAGDIQQLLQLQQLVLVPGHHLQPPAQFLLPQAQQSQPGLLP
TPNLFQLPQQTQGALLTSQPRAGLPTQPPKCLEPPSHPEEPSDLEELEQFARTFKQRRIKLGFTQGDVGL
AMGKLYGNDFSQTTISRFEALNLSFKNMCKLKPLLEKWLNDAETMSVDSSLPSPNQLSSPSLGFDGLPGR
RRKKRTSIETNVRFALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPCSAAPMLPS
PGKPASYSPHMVTPQGGAGTLPLSQASSSLSTTVTTLSSAVGTLHPSRTAGGGGGGGGAAPPLNSIPSVT
PPPPATTNSTNPSPQGSHSAIGLSGLNPSTGPGLWWNPAPYQP

>gi|7657409|ref|NP_055167.1| POU transcription factor; likely ortholog of mouse POU domain, class 2, transcription factor 3 [Homo sapiens]
MVNLESMHTDIKMSGDVADSTDARSTLSQVEPGNDRKGLDFNRQIKTEDLSDSLQQTLSHRPCHLSQGPA
MMSGNQMSGLNASPCQDMASLHPLQQLVLVPGHLQSVSQFLLSQTQPGQQGLQPNLLPFPQQQSGLLLPQ
TGPGLASQAFGHPGLPGSSLEPHLEASQHLPVPKHLPSSGGADEPSDLEELEKFAKTFKQRRIKLGFTQG
DVGLAMGKLYGNDFSQTTISRFEALNLSFKNMCKLKPLLEKWLNDAESSPSDPSVSTPSSYPSLSEVFGR
KRKKRTSIETNIRLTLEKRFQDNPKPSSEEISMIAEQLSMEKEVVRVWFCNRRQKEKRINCPVATPIKPP

VYNSRLVSPSGSLGPLSVPPVHSTMPGTVTSSCSPGNNSRPSSPGSGLHASSPTASQNNSKAAVNSASSF
NSSGSWYRWNHSTYLH

>gi|4506071|ref|NP_002731.1| protein kinase C, iota [Homo sapiens]
MSHTVAGGGSGDHSHQVRVKAYYRGDIMITHFEPSISFEGLCNEVRDMCSFDNEQLFTMKWIDEEGDPCT
VSSQLELEEAFRLYELNKDSELLIHVFPCVPERPGMPCPGEDKSIYRRGARRWRKLYCANGHTFQAKRFN
RRAHCAICTDRIWGLGRQGYKCINCKLLVHKKCHKLVTIECGRHSLPQEPVMPMDQSSMHSDHAQTVIPY
NPSSHESLDQVGEEKEAMNTRESGKASSSLGLQDFDLLRVIGRGSYAKVLLVRLKKTDRIYAMKVVKKEL
VNDDEDIDWVQTEKHVFEQASNHPFLVGLHSCFQTESRLFFVIEYVNGGDLMFHMQRQRKLPEEHARFYS
AEISLALNYLHERGIIYRDLKLDNVLLDSEGHIKLTDYGMCKEGLRPGDTTSTFCGTPNYIAPEILRGED
YGFSVDWWALGVLMFEMMAGRSPFDIVGSSDNPDQNTEDYLFQVILEKQIRIPRSLSVKAASVLKSFLNK
DPKERLGCHPQTGFADIQGHPFFRNVDWDMMEQKQVVPPFKPNISGEFGLDNFDSQFTNEPVQLTPDDDD
IVRKIDQSEFEGFEYINPLLMSAEECV

>gi|10864650|ref|NP_002735.2| protein kinase C, zeta [Homo sapiens]
MPSRTDPKMEGSGGRVRLKAHYGGDIFITSVDAATTFEELCEEVRDMCRLHQQHPLTLKWVDSEGDPCTV
SSQMELEEAFRLARQCRDEGLIIHVFPSTPEQPGLPCPGEDKSIYRRGARRWRKLYRANGHLFQAKRFNR
RAYCGQCSERIWGLARQGYRCINCKLLVHKRCHGLVPLTCRKHMDSVMPSQEPPVDDKNEDADLPSEETD
GIAYISSSRKHDSIKDDSEDLKPVIDGMDGIKISQGLGLQDFDLIRVIGRGSYAKVLLVRLKKNDQIYAM
KVVKKELVHDDEDIDWVQTEKHVFEQASSNPFLVGLHSCFQTTSRLFLVIEYVNGGDLMFHMQRQRKLPE
EHARFYAAEICIALNFLHERGIIYRDLKLDNVLLDADGHIKLTDYGMCKEGLGPGDTTSTFCGTPNYIAP
EILRGEEYGFSVDWWALGVLMFEMMAGRSPFDIITDNPDMNTEDYLFQVILEKPIRIPRFLSVKASHVLK
GFLNKDPKERLGCRPQTGFSDIKSHAFFRSIDWDLLEKKQALPPFQPQITDDYGLDNFDTQFTSEPVQLT
PDDEDAIKRIDQSEFEGFEYINPLLLSTEESV

>gi|4759124|ref|NP_004162.1| solute carrier family 1, member 2;
H.sapiens mRNA for glutamate transporter; glutamate/aspartate
transporter II; excitatory amino acid transporter 2; glial high
affinity glutamate transporter [Homo sapiens]
MASTEGANNMPKQVEVRMPDSHLGSEEPKHRHLGLRLCDKLGKNLLLTLTVFGVILGAVCGGLLRLASPI
HPDVVMLIAFPGDILMRMLKMLILPLIISSLITGLSGLDAKASGRLGTRAMVYYMSTTIIAAVLGVILVL
AIHPGNPKLKKQLGPGKKNDEVSSLDAFLDLIRNLFPENLVQACFQQIQTVTKKVLVAPPPDEEANATSA
EVSLLNETVTEVPEETKMVIKKGLEFKDGMNVLGLIGFFIAFGIAMGKMGDQAKLMVDFFNILNEIVMKL
VIMIMWYSPLGIACLICGKIIAIKDLEVVARQLGMYMVTVIIGLIIHGGIFLPLIYFVVTRKNPFSLFAG
IFQAWITALGTASSAGTLPVTFRCLEENLGIDKRVTRFVLPVGATINMDGTALYEAVAAIFIAQMNGVVL
DGGQIVTVSLTATLASVGAASIPSAGLVTMLLILTAVGLPTEDISLLVAVDWLLDRMRTSVNVVGDSFGA
GIVYHLSKSELDTIDSQHRVHEDIEMTKTQSIYDDMKNHRESNSNQCVYAAHNSVIVDECKVTLAANGKS
ADCSVEEEPWKREK

>gi|4759126|ref|NP_004163.1| solute carrier family 1 (glial high
affinity glutamate transporter), member 3 [Homo sapiens]
MTKSNGEEPKMGGRMERFQQGVRKRTLLAKKKVQNITKEDVKSYLFRNAFVLLTVTAVIVGTILGFTLRP
YRMSYREVKYFSFPGELLMRMLQMLVLPLIISSLVTGMAALDSKASGKMGMRAVVYYMTTTIIAVVIGII
IVIIIHPGKGTKENMHREGKIVRVTAADAFLDLIRNMFPPNLVEACFKQFKTNYEKRSFKVPIQANETLV
GAVINNVSEAMETLTRITEELVPVPGSVNGVNALGLVVFSMCFGFVIGNMKEQGQALREFFDSLNEAIMR
LVAVIMWYAPVGILFLIAGKIVEMEDMGVIGGQLAMYTVTVIVGLLIHAVIVLPLLYFLVTRKNPWVFIG
GLLQALITALGTSSSSATLPITFKCLEENNGVDKRVTRFVLPVGATINMDGTALYEALAAIFIAQVNNFE
LNFGQIITISITATAASIGAAGIPQAGLVTMVIVLTSVGLPTDDITLIIAVDWFLDRLRTTTNVLGDSLG
AGIVEHLSRHELKNRDVEMGNSVIEENEMKKPYQLIAQDNETEKPIDSETKM

>gi|20070239|ref|NP_006662.2| solute carrier family 1 (glutamate
transporter), member 7; excitatory amino acid transporter 5 (retinal
glutamate transporter) [Homo sapiens]
MVPHAILARGRDVCRRNGLLILSVLSVIVGCLLGFFLRTRRLSPQEISYFQFPGELLMRMLKMMILPLVV
SSLMSGLASLDAKTSSRLGVLTVAYYLWTTFMAVIVGIFMVSIIHPGSAAQKETTEQSGKPIMSSADALL
DLIRNMFPANLVEATFKQYRTKTTPVVKSPKVAPEEAPPRRILIYGVQEENGSHVQNFALDLTPPPEVVY
KSEPGTSDGMNVLGIVFFSATMGIMLGRMGDSGAPLVSFCQCLNESVMKIVAVAVWYFPFGIVFLIAGKI

LEMDDPRAVGKKLGFYSVTVVCGLVLHGLFILPLLYFFITKKNPIVFIRGILQALLIALATSSSSATLPI
TFKCLLENNHIDRRIARFVLPVGATINMDGTALYEAVAAIFIAQVNNYELDFGQIITISITATAASIGAA
GIPQAGLVTMVIVLTSVGLPTDDITLIIAVDWALDRFRTMINVLGDALAAGIMAHICRKDFARDTGTEKL
LPCETKPVSLQEIVAAQQNGCVKSVAEASELTLGPTCPHHVPVQVERDEELPAASLNHCTIQISELETNV

>gi|21314632|ref|NP_003029.2| solute carrier family 1, member 4; glutamate/neutral amino acid transporter; alanine/serine/cysteine/threonine transporter [Homo sapiens]
MEKSNETNGYLDSAQAGPAAGPGAPGTAAGRARRCAGFLRRQALVLLTVSGVLAGAGLGAALRGLSLSRT
QVTYLAFPGEMLLRMLRMIILPLVVCSLVSGAASLDASCLGRLGGIAVAYFGLTTLSASALAVALAFIIK
PGSGAQTLQSSDLGLEDSGPPPVPKETVDSFLDLARNLFPSNLVVAAFRTYATDYKVVTQNSSSGNVTHE
KIPIGTEIEGMNILGLVLFALVLGVALKKLGSEGEDLIRFFNSLNEATMVLVSWIMWYVPVGIMFLVGSK
IVEMKDIIVLVTSLGKYIFASILGHVIHGGIVLPLIYFVFTRKNPFRFLLGLLAPFATAFATCSSSATLP
SMMKCIEENNGVDKRISRFILPIGATVNMDGAAIFQCVAAVFIAQLNNVELNAGQIFTILVTATASSVGA
AGVPAGGVLTIAIILEAIGLPTHDLPLILAVDWIVDRTTTVVNVEGDALGAGILHHLNQKATKKGEQELA
EVKVEAIPNCKSEEETSPLVTHQNPAGPVASAPELESKESVL

>gi|4827012|ref|NP_005062.1| solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6; excitatory amino acid transporter 4 [Homo sapiens]
MSSHGNSLFLRESGQRLGRVGWLQRLQESLQQRALRTRLRLQTMTLEHVLRFLRRNAFILLTVSAVVIGV
SLAFALRPYQLTYRQIKYFSFPGELLMRMLQMLVLPLIVSSLVTGMASLDNKATGRMGMRAAVYYMVTTI
IAVFIGILMVTIIHPGKGSKEGLHREGRIETIPTADAFMDLIRNMFPPNLVEACFKQFKTQYSTRVVTRT
MVRTENGSEPGASMPPPFSVENGTSFLENVTRALGTLQEMLSFEETVPVPGSANGINALGLVVFSVAFGL
VIGGMKHKGRVLRDFFDSLNEAIMRLVGIIIWYAPVGILFLIAGKILEMEDMAVLGGQLGMYTLTVIVGL
FLHAGIVLPLIYFLVTHRNPFPFIGGMLQALITAMGTSSSSATLPITFRCLEEGLGVDRRITRFVLPVGA
TVNMDGTALYEALAAIFIAQVNNYELNLGQITTISITATAASVGAAGIPQAGLVTMVIVLTSVGLPTEDI
TLIIAVDWFLDRLRTMTNVLGDSIGAAVIEHLSQRELELQEAELTLPSLGKPYKSLMAQEKGASRGRGGN
ESAM

>gi|18252049|ref|NP_004161.2| solute carrier family 1, member 1; excitatory amino acid transporter-3; excitatory amino acid carrier 1 [Homo sapiens]
MGKPARKGCEWKRFLKNNWVLLSTVAAVVLGITTGVLVREHSNLSTLEKFYFAFPGEILMRMLKLIILPL
IISSMITGVAALDSNVSGKIGLRAVVYYFCTTLIAVILGIVLVVSIKPGVTQKVGEIARTGSTPEVSTVD
AMLDLIRNMFPENLVQACFQQYKTKREEVKPPSDPEMNMTEESFTAVMTTAISKNKTKEYKIVGMYSDGI
NVLGLIVFCLVFGLVIGKMGEKGQILVDFFNALSDATMKIVQIIMCYMPLGILFLIAGKIIEVEDWEIFR
KLGLYMATVLTGLAIHSIVILPLIYFIVVRKNPFRFAMGMAQALLTALMISSSSATLPVTFRCAEENNQV
DKRITRFVLPVGATINMDGTALYEAVAAVFIAQLNDLDLGIGQIITISITATSASIGAAGVPQAGLVTMV
IVLSAVGLPAEDVTLIIAVDWLLDRFRTMVNVLGDAFGTGIVEKLSKKELEQMDVSSEVNIVNPFALEST
ILDNEDSDTKKSYVNGGFAVDKSDTISFTQTSQF

>gi|5032093|ref|NP_005619.1| solute carrier family 1 (neutral amino acid transporter), member 5; neutral amino acid transporter B; RD114 virus receptor; baboon M7 virus receptor [Homo sapiens]
MVADPPRDSKGLAAAEPTANGGLALASIEDQGAAAGGYCGSRDQVRRCLRANLLVLLTVVAVVAGVALGL
GVSGAGGALALGPERLSAFVFPGELLLRLLRMIILPLVVCSLIGGAASLDPGALGRLGAWALLFFLVTTL
LASALGVGLALALQPGAASAAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEE
RNITGTRVKVPVGQEVEGMNILGLVVFAIVFGVALRKLGPEGELLIRFFNSFNEATMVLVSWIMWYAPVG
IMFLVAGKIVEMEDVGLLFARLGKYILCCLLGHAIHGLLVLPLIYFLFTRKNPYRFLWGIVTPLATAFGT
SSSSATLPLMMKCVEENNGVAKHISRFILPIGATVNMDGAALFQCVAAVFIAQLSQQSLDFVKIITILVT
ATASSVGAAGIPAGGVLTLAIILEAVNLPVDHISLILAVDWLVDRSCTVLNVEGDALGAGLLQNYVDRTE
SRSTEPELIQVKSELPLDPLPVPTEEGNPLLKHYRGPAGDATVASEKESVM

>gi|4507047|ref|NP_003036.1| solute carrier family 7 (cationic amino acid transporter, y+ system), member 1; amino acid transporter, cationic 1; ecotropic retroviral receptor [Homo sapiens]

MGCKVLLNIGQQMLRRKVVDCSREETRLSRCLNTFDLVALGVGSTLGAGVYVLAGAVARENAGPAIVISF
LIAALASVLAGLCYGEFGARVPKTGSAYLYSYVTVGELWAFITGWNLILSYIIGTSSVARAWSATFDELI
GRPIGEFSRTHMTLNAPGVLAENPDIFAVIIILILTGLLTLGVKESAMVNKIFTCINVLVLGFIMVSGFV
KGSVKNWQLTEEDFGNTSGRLCLNNDTKEGKPGVGGFMPFGFSGVLSGAATCFYAFVGFDCIATTGEEVK
NPQKAIPVGIVASLLICFIAYFGVSAALTLMMPYFCLDNNSPLPDAFKHVGWEGAKYAVAVGSLCALSAS
LLGSMFPMPRVIYAMAEDGLLFKFLANVNDRTKTPIIATLASGAVAAVMAFLFDLKDLVDLMSIGTLLAY
SLVAACVLVLRYQPEQPNLVYQMASTSDELDPADQNELASTNDSQLGFLPEAEMFSLKTILSPKNMEPSK
ISGLIVNISTSLIAVLIITFCIVTVLGREALTKGALWAVFLLAGSALLCAVVTGVIWRQPESKTKLSFKV
PFLPVLPILSIFVNVYLMMQLDQGTWVRFAVWMLIGFIIYFGYGLWHSEEASLDADQARTPDGNLDQCK

>gi|4507049|ref|NP_003037.1| solute carrier family 7 (cationic amino acid transporter, y+ system), member 2; amino acid transporter, cationic 2 [Homo sapiens]
MIPCRAALTFARCLIRRKIVTLDSLEDTKLCRCLSTMDLIALGVGSTLGAGVYVLAGEVAKADSGPSIVV
SFLIAALASVMAGLCYAEFGARVPKTGSAYLYTYVTVGELWAFITGWNLILSYVIGTSSVARAWSGTFDE
LLSKQIGQFLRTYFRMNYTGLAEYPDFFAVCLILLLAGLLSFGVKESAWVNKVFTAVNILVLLFVMVAGF
VKGNVANWKISEEFLKNISASAREPPSENGTSIYGAGGFMPYGFTGTLAGAATCFYAFVGFDCIATTGEE
VRNPQKAIPIGIVTSLLVCFMAYFGVSAALTLMMPYYLLDEKSPLPVAFEYVGWGPAKYVVAAGSLCALS
TSLLGSMFPLPRILFAMARDGLLFRFLARVSKRQSPVAATLTAGVISALMAFLFDLKALVDMMSIGTLMA
YSLVAACVLILRYQPGLSYDQPKCSPEKDGLGSSPRVTSKSESQVTMLQRQGFSMRTLFCPSLLPTQQSA
SLVSFLVGFLAFLVLGLSVLTTYGVHAITRLEAWSLALLTLFLVLFVAIVLTIWRQPQNQQKVAFMVPFL
PFLPAFSILVNIYLMVQLSADTWVRFSIWMAIGFLIYFSYGIRHSLEGHLRDENNEEDAYPDNVHAAAEE
KSAIQANDHHPRNLSSPFIFHEKTSEF

>gi|17939406|ref|NP_116192.2| solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 [Homo sapiens]
MPWQAFRRFGQKLVRRRTLESGMAETRLARCLSTLDLVALGVGSTLGAGVYVLAGEVAKDKAGPSIVICF
LVAALSSVLAGLCYAEFGARVPRSGSAYLYSYVTVGELWAFTTGWNLILSYVIGTASVARAWSSAFDNLI
GNHISKTLQGSIALHVPHVLAEYPDFFALGLVLLLTGLLALGASESALVTKVFTGVNLLVLGFVMISGFV
KGDVHNWKLTEEDYELAMAELNDTYSLGPLGSGGFVPFGFEGILRGAATCFYAFVGFDCIATTGEEAQNP
QRSIPMGIVISLSVCFLAYFAVSSALTLMMPYYQLQPESPLPEAFLYIGWAPARYVVAVGSLCALSTSLL
GSMFPMPRVIYAMAEDGLLFRVLARIHTGTRTPIIATVVSGIIAAFMAFLFKLTDLVDLMSIGTLLAYSL
VSICVLILRYQPDQETKTGEEVELQEEAITTESEKLTLWGLFFPLNSIPTPLSGQIVYVCSSLLAVLLTA
LCLVLAQWSVPLLSGDLLWTAVVVLLLLLIIGIIVVIWRQPQSSTPLHFKVPALPLLPLMSIFVNIYLMM
QMTAGTWARFGVWMLIGFAIYFGYGIQHSLEEIKSNQPSRKSRAKTVDLDPGTLYVHSV

>gi|29789100|ref|NP_061325.1| similar to glucosamine-6-sulfatases; sulfatase 2 [Homo sapiens]
MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQVMNKTRRI
MEQGGAHFINAFVTTPMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHESRTFAVYLNSTGYRTAF
FGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSKDYLTDLITNDSVSFFRTSKKM
YPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQ
RKRLQTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNV
EAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLL
HKRDNDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALS
NLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPR
NLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKSLQAWKDHKLH
IDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSLHPFRKGLQEKDKVWLLRE
QKRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNNTYWCMRTINETHNFL
FCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNPRTRNMDLGLKDGGSYE
QYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

>gi|29789064|ref|NP_055985.1| sulfatase FP [Homo sapiens]
MKYSCCALVLAVLGTELLGSLCSTVRSPRFRGRIQQERKNIRPNIILVPTDDQDVELGSLQVMNKTRKIM
EHGGATFINAFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAFF
GKYLNEYNGSYIPPGWREWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLITNESINYFKMSKRMY
PHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSYNYAPNMDKHWIMQYTGPMLPIHMEFTNILQR

KRLQTLMSVDDSVERLYNMLVETGELENTYIIYTADHGYHIGQFGLVKGKSMPYDFDIRVPFFIRGPSVE
PGSIVPQIVLNIDLAPTILDIAGLDTPPDVDGKSVLKLLDPEKPGNRFRTNKKAKIWRDTFLVERGKFLR
KKEESSKNIQQSNHLPKYERVKELCQQARYQTACEQPGQKWQCIEDTSGKLRIHKCKGPSDLLTVRQSTR
NLYARGFHDKDKECSCRESGYRASRSQRKSQRQFLRNQGTPKYKPRFVHTRQTRSLSVEFEGEIYDINLE
EEEELQVLQPRNIAKRHDEGHKGPRDLQASSGGNRGRMLADSSNAVGPPTTVRVTHKCFILPNDSIHCER
ELYQSARAWKDHKAYIDKEIEALQDKIKNLREVRGHLKRRKPEECSCSKQSYYNKEKGVKKQEKLKSHLH
PFKEAAQEVDSKLQLFKENNRRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPFWNLGSFCACTS
SNNNTYWCLRTVNETHNFLFCEFATGFLEYFDMNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQ
CNPRPKNLDVGNKDGGSYDLHRGQLWDGWEG

>gi|27597096|ref|NP_775491.1| uridine phosphorylase-2; liver-specific uridine phosphorylase [Homo sapiens]
MASVIPASNRSMRSDRNTYVGKRFVHVKNPYLDLMDEDILYHLDLGTKTHNLPAMFGDVKFVCVGGSPNR
MKAFALFMHKELGFEEAEEDIKDICAGTDRYCMYKTGPVLAISHGMGIPSISIMLHELIKLLHHARCCDV
TIIRIGTSGGIGIAPGTVVITDIAVDSFFKPRFEQVILDNIVTRSTELDKELSEELFNCSKEIPNFPTLV
GHTMCTYDFYEGQGRLDGALCSFSREKKLDYLKRAFKAGVRNIEMESTVFAAMCGLCGLKAAVVCVTLLD
RLDCDQINLPHDVLVEYQQRPQLLISNFIRRRLGLCD

>gi|4507839|ref|NP_003355.1| uridine phosphorylase [Homo sapiens]
MAATGANAEKAESHNDCPVRLLNPNIAKMKEDILYHFNLTTSRHNFPALFGDVKFVCVGGSPSRMKAFIR
CVGAELGLDCPGRDYPNICAGTDRYAMYKVGPVLSVSHGMGIPSISIMLHELIKLLYYARCSNVTIIRIG
TSGGIGLEPGTVVITEQAVDTCFKAEFEQIVLGKRVIRKTDLNKKLVQELLLCSAELSEFTTVVGNTMCT
LDFYEGQGRLDGALCSYTEKDKQAYLEAAYAAGVRNIEMESSVFAAMCSACGLQAAVVCVTLLNRLEGDQ
ISSPRNVLSEYQQRPQRLVSYFIKKKLSKA

>gi|5803133|ref|NP_006825.1| RAB32, member RAS oncogene family [Homo sapiens]
MAGGGAGDPGLGAAAAPAPETREHLFKVLVIGELGVGKTSIIKRYVHQLFSQHYRATIGVDFALKVLNWD
SRTLVRLQLWDIAGQERFGNMTRVYYKEAVGAFVVFDISRSSTFEAVLKWKSDLDSKVHLPNGSPIPAVL
LANKCDQNKDSSQSPSQVDQFCKEHGFAGWFETSAKDNINIEEAARFLVEKILVNHQSFPNEENDVDKIK
LDQETLRAENKSQCC

>gi|11641237|ref|NP_071732.1| RAB38; Rab-related GTP-binding protein [Homo sapiens]
MQAPHKEHLYKLLVIGDLGVGKTSIIKRYVHQNFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQE
RFGNMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNGKPVSVVLLANKCDQGKDVLMNNG
LKMDQFCKEHGFVGWFETSAKENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASCSGCAK
S

>gi|4506375|ref|NP_003920.1| RAB7, member RAS oncogene family-like 1 [Homo sapiens]
MGSRDHLFKVLVVGDAAVGKTSLVQRYSQDSFSKHYKSTVGVDFALKVLQWSDYEIVRLQLWDIAGQERF
TSMTRLYYRDASACVIMFDVTNATTFSNSQRWKQDLDSKLTLPNGEPVPCLLLANKCDLSPWAVSRDQID
RFSKENGFTGWTETSVKENKNINEAMRVLIEKMMRNSTEDIMSLSTQGDYINLQTKSSSWSCC

>gi|8923042|ref|NP_060103.1| chromosome 6 open reading frame 37; retinal expressed gene C6orf37 [Homo sapiens]
MAEGEGYFAMSEDELACSPYIPLGGDFGGGDFGGGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNV
LNWEQVQRLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVRDVRLNGSAASHVLHQDSGL
GYKDLDLIFCADLRGEGEFQTVKDVVLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLIS
LSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSENPMTETFHPTIIGESVYGDFQEAFDHL
CNKIIATRNPEEIRGGGLLKYCNLLVRGFRPASDEIKALQRYMCSRFFIDFSDIGEQQRKLESYLQNHFV
GLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNLITMLAIRVLADQNVIPNVANVTCYYQPAPYVADAN
FSNYYIAQVQPVFTCQQQTYSTWLPCN

>gi|8923192|ref|NP_060179.1| hypothetical protein FLJ20202 [Homo sapiens]

MAEESSCTRDCMSFSVLNWDQVSRLHEVLTEVVPIHGRGNFPTLEITLKDIVQTVRSRLEEAGIKVHDVR
LNGSAAGHVLVKDNGLGCKDLDLIFHVALPTEAEFQLVRDVVLCSLLNFLPEGVNKLKISPVTLKEAYVQ
KLVKVCTDTVRWSLISLSNKNGKNVELKFVDSIRRQFEFSVDSFQIILDSLLFFYDCSNNPISEHFHPTV
IGESMYGDFEEAFDHLQNRLIATKNPEEIRGGGLLKYSNLLVRDFRPTDQEEIKTLERYMCSRFFIDFPD
ILEQQRKLETYLQNHFAEEERSKYDYLMILRRVVNESTVCLMGHERRQTLNLISLLALRVLAEQNIIPSA
TNVTCYYQPAPYVSDGNFSNYYVAHPPVTYSQPYPTWLPCN

>gi|16418427|ref|NP_443175.1| hypothetical protein MGC16491 [Homo sapiens]
MPSESGAERRDRAAAQVGTAAATAVATAAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIH
GRGNFPTLSVQPRQIVQVVRSTLEEQGLHVHSVRLHGSAASHVLHPESGLGYKDLDLVFRVDLRSEASFQ
LTKAVVLACLLDFLPAGVSRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVELKFVDSVRRQ
FEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTGESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLK
YCHLLVRGFRPRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGADAARRYACLVTLHRVVN
ESTVCLMNHERRQTLDLIAALALQALAEQGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTW
LPCN

>gi|22749287|ref|NP_689843.1| hypothetical protein MGC26999 [Homo sapiens]
MSEIRFTNLTWDQVITLDQVLDEVIPIHGKGNFPTMEVKPKDIIHVVKDQLIGQGIIVKDARLNGSVASY
ILASHNGISYKDLDVIFGVELPGNEEFQVVKDAVLDCLLDFLPKDVKKEKLSPDIMKDAYVQKLVKVCNG
HDCWSLISLSNNTGKNLELKFVSSLRRQFEFSVDSFQIVLDPMLDFYSDKNAKLTKESYPVVVAESMYGD
FQEAMTHLQHKLICTRKPEEIRGGGLLKYCSLLVHGFKPACMSEIKNLERYMCSRFFIDFPHIEEQQKKI
ESYLHNHFIGEGMTKYDYLMTLHGVVNESTVCLMSYERRQILHLITMMALKVLGELNILPNTQKVTCFYQ
PAPYFAAEARYPIYVIPEPPPVSFQPYHPLHFRGSNGMS

WHAT IS CLAIMED IS:

1. A method of identifying a candidate beta-catenin pathway modulating agent, said method comprising the steps of:

(a) providing an assay system comprising a MBCAT polypeptide or nucleic acid;

(b) contacting the assay system with a test agent under conditions whereby, but for the presence of the test agent, the system provides a reference activity; and

(c) detecting a test agent-biased activity of the assay system, wherein a difference between the test agent-biased activity and the reference activity identifies the test agent as a candidate beta-catenin pathway modulating agent.

2. The method of Claim 1 wherein the assay system comprises cultured cells that express the MBCAT polypeptide.

3. The method of Claim 2 wherein the cultured cells additionally have defective beta-catenin function.

4. The method of Claim 1 wherein the assay system includes a screening assay comprising a MBCAT polypeptide, and the candidate test agent is a small molecule modulator.

5. The method of Claim 4 wherein the assay is a binding assay.

6. The method of Claim 1 wherein the assay system is selected from the group consisting of an apoptosis assay system, a cell proliferation assay system, an angiogenesis assay system, and a hypoxic induction assay system.

7. The method of Claim 1 wherein the assay system includes a binding assay comprising a MBCAT polypeptide and the candidate test agent is an antibody.

8. The method of Claim 1 wherein the assay system includes an expression assay comprising a MBCAT nucleic acid and the candidate test agent is a nucleic acid modulator.

9. The method of claim 8 wherein the nucleic acid modulator is an antisense oligomer.

10. The method of Claim 8 wherein the nucleic acid modulator is a PMO.

11. The method of Claim 1 additionally comprising:

(d) administering the candidate beta-catenin pathway modulating agent identified in (c) to a model system comprising cells defective in beta-catenin function and, detecting a phenotypic change in the model system that indicates that the beta-catenin function is restored.

12. The method of Claim 11 wherein the model system is a mouse model with defective beta-catenin function.

13. A method for modulating a beta-catenin pathway of a cell comprising contacting a cell defective in beta-catenin function with a candidate modulator that specifically binds to a MBCAT polypeptide, whereby beta-catenin function is restored.

14. The method of claim 13 wherein the candidate modulator is administered to a vertebrate animal predetermined to have a disease or disorder resulting from a defect in beta-catenin function.

15. The method of Claim 13 wherein the candidate modulator is selected from the group consisting of an antibody and a small molecule.

16. The method of Claim 1, comprising the additional steps of:

(d) providing a secondary assay system comprising cultured cells or a non-human animal expressing MBCAT ,

(e) contacting the secondary assay system with the test agent of (b) or an agent derived therefrom under conditions whereby, but for the presence of the test agent or agent derived therefrom, the system provides a reference activity; and

(f) detecting an agent-biased activity of the second assay system,

wherein a difference between the agent-biased activity and the reference activity of the second assay system confirms the test agent or agent derived therefrom as a candidate beta-catenin pathway modulating agent,

and wherein the second assay detects an agent-biased change in the beta-catenin pathway.

17. The method of Claim 16 wherein the secondary assay system comprises cultured cells.

18. The method of Claim 16 wherein the secondary assay system comprises a non-human animal.

19. The method of Claim 18 wherein the non-human animal mis-expresses a beta-catenin pathway gene.

20. A method of modulating beta-catenin pathway in a mammalian cell comprising contacting the cell with an agent that specifically binds a MBCAT polypeptide or nucleic acid.

21. The method of Claim 20 wherein the agent is administered to a mammalian animal predetermined to have a pathology associated with the beta-catenin pathway.

22. The method of Claim 20 wherein the agent is a small molecule modulator, a nucleic acid modulator, or an antibody.

23. A method for diagnosing a disease in a patient comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the sample with a probe for MBCAT expression;

(c) comparing results from step (b) with a control;

(d) determining whether step (c) indicates a likelihood of disease.

24. The method of claim 23 wherein said disease is cancer.

ABSTRACT OF THE DISCLOSURE

Human MBCAT genes are identified as modulators of the beta-catenin pathway, and thus are therapeutic targets for disorders associated with defective beta-catenin function. Methods for identifying modulators of beta-catenin, comprising screening for agents that modulate the activity of MBCAT are provided.